M. Boin

	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	
OM protein - pro	OM protein - protein search, using sw model	
Run on:	June 10, 2002, 17:14:13 ; Search time 29.79 Seconds (without alignments) 894.854 Million cell updates/sec	
Title: Perfect score: Sequence:	US-09-297-171-1 1304 1 NGDRLYRADSRPPDEIKRSGQIFSDYQSEVDIYNRIRDEL 240	
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5	
Searched:	747574 segs, 111073796 residues	
Total number of	Total number of hits satisfying chosen parameters: 747574	
Minimum DB seq.	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	
Post-processing	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database :	A_Geneseq_032802:* 1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:* 2: /GTG1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*	

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| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:\*
| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*
| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 

SUMMARIES	
SUM	
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Result		& Query	•		!	
Q	Score	Match	Match Length DB ID	08	QI	Description
п	1304	100.0	258	9	AAP50190	Sequence encoded b
7	1298	99.5		9	AAP50191	Sequence encoded b
m	1298	99.5	382	22	AAU00506	E. coli heat-labil
4	1293	99.5		19	AAW65074	E. coli LT-A prote
ហ	1288	98.8		19	AAW65075	E. coli LT-A mutan
9	1287	98.7		21	AAY96646	Plant-optimized E.
7	1283	98.4		21	AAY96647	Synthetic E. coli
80	1282	98.3		21	AAY96649	Plant-optimized E.
6	1280	98.2		21	AAY96648	Plant-optimized E.
10	1280	98.2		22	AAU00507	E. coli heat-labil
11	1276	97.9		21	AAY96650	Plant-optimized E.

Plant-optimized E.	E. coli heat labil	E.coli heat labile	Peptide sequence f		Glu-114" E.col	4" E	± π	" E.col	" E.col	33" E.col	E.	<u> </u>	"Ser-106" E.coli h	E.col1	Ser-104" E.col	" E.coli	Cholera toxin subu	Amino acid sequenc	Plant-optimized V.	Cholera toxin A su	Plant-optimized mu	Cholera toxin subu	Cholera toxin Al f	Lys-63 cholera tox	Glu-114 cholera to	Plant-optimized mu	Ser-110 cholera to	Lys-97 cholera tox	-112	9	3 cholera	Plant-optimized mu	Ser-106 cholera to
AAY96651	AAW67772	AAR38728	AAU14105	AAR44016	AAR44024	AAR44025	AAR44018	AAR38732	AAR44017	AAR38731	AAR38730	AAR44019	AAR44023	AAR44020	AAR44022	AAR44021	AAR38729	AAW80807	AAY96653	AAG65991	AAY96655	AAW67773	AAR13117	02	AAR44033	AAY96654	03	AAR44028	3	AAR44030	2	AAY96656	2
21	20	14	22	14	14	14	14	14	14	14	14	14	14	14	14	14	14	19	21	22	21	20	12	14	14	21	14	14	14	14	14	21	14
259	237	236	254	236	236	236	236	236	236	236	236	236	236	236	236	236	240	240	258	258	258	240	258	240	240	258	240	240	240	240	240	258	240
	91.3			90.4	90.4	90.4	90.3	90.3		90.3		90.1		0.06		0.06	83.4	83.4	83.4	83.4		83.2										82.9	
1275	1190.5	1183	1183	1179	1179	1179	1178	1178	1177	1177	1176	1175	1175	1174	1174	1173	1088		1088	1088	1087	1085	1085	1084	1084	1084	1083	1082	1082	1081	1081	1081	1080
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30.	31			34			37	38	39	40	41	42	43	44	45

## ALIGNMENTS

ULT 1	Sequence encoded by the pig scours heat labile toxin (LT) LTA gene. Pig scours vaccine; toxin; diarrhoea. E.coli NCIB 11932.	EP145486-A. 19-JUN-1985.	12-DEC-1984; 84EP-0308620. 12-DEC-1983; 83GB-0033131. (GLAX ) GLAXO GROUP LTD. Hayes MV, Harford S, Ross GW;	WPI; 1985-148358/25. N-PSDB; AAN50205. New toxoid as inactivated form of toxin for use in vaccines - is obcd. from organism transformed by gene Disclosure; Fig 1; 61pp; English.
RESULT TID AAP5 XX XX AC AAP5 XX XX XX XX XX XX XX XX				

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AANSO205 is the gene sequence of the natural LTA gene. The LTA gene of the site directed mutant SDM1 (see AANSO206) is inactive. The inventors claim a vaccine prepn. active against pig scours which contains an inactivated LTA component, together with additional K88 antigens opt. with whole cells comprising the antigens or contg. the inactivated LTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AANSO205 is the gene sequence of the natural LTA gene. The LTA gene of the site directed mutant SDM1 (see AANSO206) is inactive. The inventors claim a vaccine prepn. active against pig scours which
                                                                                                                                                                                                                   121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                                                                              STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                         Gaps
                                                                                                                                                            1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
                                                                                                                                                                                   78
                                                                                                                                                                                                                                                                                                                                                                                                                                     scours heat labile toxin (LT) LTA gene SDM1.
                                                                                                                                                                        HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL
                                                                                                                                         .;
0
                                                                                                                   Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccines
                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use in
                                                                                                                Query Match 100.0%; Score 1304; DB 6; Best Local Similarity 100.0%; Pred. No. 2.9e-127; Matches 240; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New toxoid as inactivated form of toxin for obtd. from organism transformed by gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Ser in native SQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pig scours vaccine; toxin; diarrhoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 79
                                                                                                                                                                                                                                                                                                                                                                               AA.
                                                                                                                                                                                                                                                                                                                                                                            AAP50191 standard; Protein; 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Fig 2; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence encoded by the pig
of the site directed mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ross
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84EP-0308620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83GB-0033131
                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harford S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1985-148358/25.
N-PSDB; AAN50206.
                                                                               258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E.coli NCIB 11932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                       30-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-DEC-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-DEC-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUN-1985.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP145486-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayes MV,
                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                   AAP50191;
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Matches
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YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                                                                                                     HHAPQGCGNSSRIIGDICNEETQNLSIIVLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
                                                                                                                                                                                      STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                   Gaps
Contains≯an inactivated LTA component, together with additional K88 antigens opt. with whole cells comprising the antigens or contg. the inactivated LTA.
                                                                                                                                                    1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heat-labile enterotoxin; LT; LTS63Y; LTdel110/112; mutant;
detoxified and immunologically active protein; ADP-ribosylation; Gs;
endotoxin; diarrhoea; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Important residue for enzymatic activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "Important residue for enzymatic activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Important residue for enzymatic activity'
                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Substitution of wild type Ser to Tyr"
                                                                                       Length 258;
                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Important residue for enzymatic
259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Important residue for enzymatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                    E. coli heat-labile enterotoxin (LT) mutant LTS63Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the NAD-binding site"
                                                                                    Score 1298; DB 6;
Pred. No. 1.2e-126;
                                                                                                   Pred. No. 1.26
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Encoded by TG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                           AAU00506 standard; Protein; 382 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli strain K88ac
                                                                                    99.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-KR00555
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= 72
58..72
/note= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note=
                                                                                                 Best Local Similarity
Matches 239; Conserv
                                                 258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     AAU00506;
                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                              199
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AAW65075;
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                                                                                                                                                              The present sequence represents Escherichia coll heat-labile enterotoxin (LT) mutant LTS63Y. LTS63Y and LTdell10/112 (AAU00507)

are two novel detoxified and immunologically active proteins (LT mutants) derived by site-directed mutagenesis of the Al subunit of wild type LT. The substitution of Ser to Tyr at position 63 in LTS63Y blocks (AAD-binding. Deletion of Glu residues at position 63 in LTS63Y blocks (AAD-binding. Deletion of Glu residues at positions 110 and 112 in LTGell10/112 eliminate the enzymatic activity of LT. The Al subunit of wild type LT catalyses APD-ribosylation of Gs, a GTP-binding protein that regulates CAMP levels. The resulting increase in CAMP is the cause of darrhoea in humans and animals e.g. pags. The mucosal immunogenicities of mutant heat-labile endotoxins 17563Y and 17dell10/112 The control Groups of mice were immunised with LTS63Y or LTdell10/112. The control faccal antibody titres to LT were determined. The results showed that comparable level of anti-LT antibodies in sera and faccal extracts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                ייסי שבעסגווופס mutants of Escherichia coli heat-labile enterotoxin
useful as vaccine for preventing and treating diarrhoea, and as adjuvant
for antibody production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heat labile toxin subunit A; LT-A; mutant; immunogen; detoxification; carrier; adjuvant; prevention; treatment; disease; diarrhoea; vaccine; infection; enterotoxic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    compared with those immunised with wild-type LT. The LT mutants are useful as a vaccine for preventing and treating diarrhoea and as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1298; DB 22;
Pred. No. 2.2e-126;
0; Mismatches 1;
 Chung S;
 Yum J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 1..241
                                                                                                                                      Claim 2; Page 39-41; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW65074 standard; protein; 240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    adjuvant for antibody production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E. coli LT-A protein fragment.
Chang J,
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99.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                              WPI; 2001-281524/29.
N-PSDB; AAS01505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 239; Conserv
 Kim JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
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 ЕJ,
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Protein
 Park
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immunogenic compositions, optionally comprising an adjuvant and/or a second immunogenic antigen. Such compositions can be administered to prevent/treat disease in a subject e.g. traveller's diarrhoea in humans. The protein or compositions are especially administered as vaccines useful to prevent or treat infections by enterotoxigenic strain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a fragment of an Escherichia coil heat labile toxin subunit A (LT-A). This protein is used in a method resulting in a mutant LT-A protein which has the wild type Ala residue at position 72 changed to an Arg residue resulting in a toxin which retains its immunogenicity but is detoxified. Detoxification is defined in the specification as a reduction in toxicity relative to wild type toxin, such that any residual toxicity is sufficiently low to allow use as an effective immunogenic composition in humans without significant side effects. The protein can be combined with an acceptable carrier in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mutated Escherichia coli heat labile toxin subunit A - is immunogenic and detoxified relative to wild-type, useful e.g. in vaccines against E. coli enterotoxigenic strains and as an adjuvant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1293; DB 19;
Pred. No. 3.7e-126;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E. coli LT-A mutant A72R protein fragment.
/note- "partial sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coli in mammals (especially humans)
                                                                                                                                                                                                                                                                                                                                       Rappuoli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW65075 standard; protein; 240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page -; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.2%;
                                                                                                                                                                   97WO-IB01440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.2'
Matches 238; Conservative
                                                                                                                                                                                                                                                                                                                                       Pizza M,
                                                                                                                                                                                                                                                                                 (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 AA;
                                                                                                                                                                                                                                                                                                                                       Giuliani MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11, SEP-1999
                                                  WO9818928-A1
                                                                                                                                                                30-0CT-1997;
                                                                                                           07-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXEXEXEX
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MAY96646>standard; Protein; 259 AA.

(first entry)

26-SEP-2000

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 carrier; adjuvant; prevention; treatment; disease; diarrhoea; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 STSLSLRSAHLAGOSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E. coli in mammals (especially humans).
NOTE: This sequence does not appear in the specification but has
been constructed from the wild-type sequence represented in AAW65074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
                                                                                                                                                                                                                                                                                                                                                                                                    Mutated Escherichia coli heat labile toxin subunit A - is immunogenic and detoxified relative to wild-type, useful e.g. in vaccines against E. coli enterotoxigenic strains and as an adjuvant
                                                                                                                /label- A72R
/note= "Wild type Ala residue is replaced by Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1288; DB 19;
Pred. No. 1.2e-125;
1; Mismatches 2;
                                                                        ...,
Misc-difference 72
                                                                                                                                                                                                                                                                                                                                        Rappuoli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page -; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.8%;
98.8%;
                                                                                                                                                                                                                                     97WO-IB01440.
                                                                                                                                                                                                                                                                      96GB-0022660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237; Conservative
                 infection; enterotoxic.
                                                                                                                                                                                                                                                                                                                                    Giuliani MM, Pizza M,
                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-272223/24.
                                                                                                                                                                                                                                                                                                       (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 AA
                                                Escherichia coli
                                                                                                                                                                                                                                     30-OCT-1997;
                                                                                                                                                                                                                                                                      31-OCT-1996;
                                                                                                                                                                   WO9818928-A1
                                                                                                                                                                                                    07-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Matches
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RESULT AAY96646

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interpretation optimized CDRA. The recorded by a plant-condon optimized CDRA. The condon optimized CDRA. The condon optimized CDRA sequence contains plant-preferred codons and eliminates sequence motifs associated with sprucessing. A single codon insertion (GTG encoding valine) was made to accomcdate the creation of a NCoI restriction site around the initiator methionine codon. Novel polynucleotides encode a mutant LT-A polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible prophylactic or therapeutic treatment against B. coli or V. cholerae. The mutant polypeptides are also useful as adjuvants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                     Heat-labile toxin; LT-B; mutant; transgenic plant; vaccine; oral; adjuvant; anti-bacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This synthetic Escherichia coli heat-labile toxin (LT) A subunit (LT-A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STSLSLRSAHLAGQSILSGYSTYXIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 ngdklyradsrppdeikrsgglmprghneyfdrgtqmninlydhargtqtgfvryddgyv 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.7%; Score 1287; DB 21; Length 259; 98.3%; Pred. No. 1.7e-125;
                                                                                                                                                                                                   Plant-optimized E. coli heat labile toxin A subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.7e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1..18
/label= signal_peptide
19..259
/label= mature_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 1; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mason HS, Arntzen CJ;
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(ARNT/) ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-442653/38.
N-PSDB; AAA51106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 236; Conserv
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                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200037609-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
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WPI; 2000-442653/38.
N-PSDB; AAA51545.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                        AAY96649;
                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is mutant S63K Escherichia coli heat-labile toxin (LT) A subunit (LT-A). The wild-type serine was replaced with lysine at residue 63 of the mature protein, which was caused by a codon change of TCC to AAG in the coding sequence. The sequence contains plant-preferred codons and eliminates sequence motifs associated with spurious mRNA processing. A single codon insertion (GTG encoding valine) was made to accomodate the creation of a NcoI restriction site around the initiator methionine codon. Novel polynucleotides encode a mutant LT-A polypeptide or a mutant vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The
                                                                                                                                                                                                                          Heat-labile toxin; LT-A; LT-B; mutein; transgenic plant; vaccine; oral;
                                stslslrsahlaggsilsgystyyiyviatapnmfnvndvlgvysphpyegevsalggip 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals
                                                            YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI
                                                                                                                                                                                                                                                                                                                                                                 /label- S63K
/note- "Wild-type serine is replaced by lysine"
                                                                                                                                                                                                                                                                                         Location/Qualifiers
1..19
/label= signal_peptide
/note= "20"
                                                                                                                                                                                                                                                                                                                                 20..259
7abel- mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BOYC-) BOYCE THOMPSON INST PLANT RES
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                                                                                                                                                                                                     Synthetic E. coli LT-A K63 mutant.
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                                                                                                                                      AAY96647 standard; Protein; 259
                                                                                                                                                                                                                                     adjuvant; anti-bacterial; S63K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0113507.
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                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mason HS, Arntzen CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ARNT/) ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-442653/38.
N-PSDB; AAA51147.
                                                                                                                                                                                                                                                         Escherichia coli
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                                                                                                                                                                                                                                                                    Synthetic
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                                                                                                                                                                                                                                                                                                    Peptide
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polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible vaccines, especially oral vaccines in transgenic plants for the prophylactic or therapeutic treatment against E. coll or V. cholerae. The mutant polypeptides are also useful as adjuvants.

NB: This sequence does not appear in the specification, it was made from the wild type sequence shown in AAY96647, which appears in Figure 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat-labile toxin, LT-8, LT-B, mutant, transgenic plant, vaccine, oral, adjuvant, anti-bacterial, A72R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          20 ngdklyradsrppdelkrsgglmprghneyfdrgtgmninlydhargtgtgfvryddgyv 79
                                                                                                                                                                                                                                                                                                                                                                                  1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label- A72R
/note= "Wild type alanine is replaced by arginine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL
                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                              Length 259;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                            Score 1283; DB 21;
Pred. No. 4.5e-125;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant-optimized E. coli LT-A R72 mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20..259
/label- mature_protein
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(MASO/) MASON H S.
(ARNI/) ARNIZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY96649 standard; Protein; 259 AA
                                                                                                                                                                                                                                                                              98.4%;
97.9%;
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                                                                                                                                                                                                                                                                                                                                Matches 235; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mason HS, Arntzen CJ;
                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                       259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
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/label= mature\_protein

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61
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                                                                                           This is muchan. Also Explained with arginine at residue 72 of the mature protein, which was caused by a nucleotide change of GC to GC the mature protein, which was caused by a nucleotide change of GC to GC the mature protein, which was caused by a nucleotide change of GC to GC the mature protein, which was caused by a nucleotide change of GC to be an arginial sequence motifs associated with spurious mRNA processing. A single codon insertion (GTG encoding valine) was made to accomodate the creation of a Noor restriction site around the initiator methionine codon. Novel polynucleotides encode a mutant U.T.A polypeptide or a mutant vibrio cholerae cholera toxin (CT) a subunit (GT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or GT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide are useful for the cumprises a nucleic acid sequence encoding LT-B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transgenic plants to produce edible vaccines, especially oral vaccines in transgenic plants to cholerae. The mutant polypeptides are also useful as adjuvants.

Constructed from the wild type LT-A shown in AAV96646 which is given in Figure 1 of the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutant; transgenic plant; vaccine; oral;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
transformation of plant cells, useful in immunogenic compositions elicit immune responses in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 97.9%; Pred. No. 5.7e-125;
Matches 235; Conservative 4; Mismatchee 1: Table 2.35
                                                                                     This is mutant A72R Escherichia coli heat-labile toxin (LT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant-optimized E. coli LT-A G192 mutant.
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/label= signal_peptide
20..259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY96648 standard; Protein; 259 AA
                                                            Example 4; Page -; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heat-labile toxin; LT-A; LT-B; m
adjuvant; anti-bacterial; R192G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                               259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                 Seguence
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This is mutant R192G Escherichia coli heat-labile toxin (LT) A subunit (LT-A). The wild-type arginine was replaced with glycine at residue 192 of the mature protein, which was caused by a codon change of TCC to AAG in the coding sequence. The sequence contains plant-preferred codons and single codon insertion (GTG encoding value) was made to accomodate the creation of a NCOI restriction site around the initiator methionine codon. Novel polynucleotides encode a mutant LT-A polypeptide or a mutant vibrio cholerae cholera toxin (CT) A subunit (GT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic coil sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the prophylactic or therapeutic cord and transgenic plants for the prophylactic or therapeutic cord meant against E. Coli or V. cholerae. The mutant polypeptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NB: This sequence does not appear in the specification, it was made the wild type sequence shown in AAY96647, which appears in Figure 1.
                                                               /note= "Wild-type arginine is replaced by glycine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Pred. No. 9.3e-125;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                 (BOYC-) BOYCE THOMPSON INST PLANT RES (MASO/) MASON H S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page -; 103pp; English.
                               /label= R192G
                                                                                                                                                                                                                                                 99WO-US30747.
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Best Local Similarity 97.9%;
Matches 235; Conservative
                                                                                                                                                                                                                                                                                                          98US-0113507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              also useful as adjuvants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mason HS, Arntzen CJ;
                                                                                                                                                                                                                                                                                                                                                                                                (MASO/) MASON H S.
(ARNI/) ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-442653/38.
Misc-difference 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAA51544.
                                                                                                                        WO200037609-A2
                                                                                                                                                                                                                                              22-DEC-1999;
                                                                                                                                                                                                                                                                                                          22-DEC-1998;
                                                                                                                                                                                     29-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New detoxified mutants of Escherichia coli heat-labile enterotoxin useful as vaccine for preventing and treating diarrhoea, and as adjuvant for antibody production
                                                                                                                                                                                                                   Heat-labile enterotoxin; LT; LTS63Y; LTdell110/112; mutant; detoxified and immunologically active protein; ADP-ribosylation; Gs; endotoxin; diarrhoea; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                          'note⇒ "Important residue for enzymatic activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Important residue for enzymatic activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Important residue for enzymatic activity"
                                                                                                                                                                           E. coli heat-labile enterotoxin (LT) mutant LTdell10/112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Forms the NAD-binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Encoded by TG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yum J,
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                            AAU00507 standard; Protein; 380 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adjuvant for antibody production.
                                                                                                                                                                                                                                                                                                                Escherichia coli strain K88ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eark EJ, Kim JS, Chang J,
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                                                                                                                                 (first entry)
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N-PSDB; AAS01506.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200119998-A1
                                                                                                                                                                                                                                                                                                                                                                                 Key
Misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-ŠEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc_feature
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                                                                                                                                 29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAR-2001
                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                   AAU00507;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
RESULT 10
                    AAU00507
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Heat-labile toxin; LT-B; LT-B; mutant; transgenic plant; vaccine; oral; adjuvant; anti-bacterial; A63K+R192G; double mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- R192G
/note- "the wild type arginine is replaced by glycine
at position 192 of the mature sequence"
                                                                                                       121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                           61 STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                          Gaps
                                                          New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "the wild type serine is replaced by lysine at position 63 of the mature sequence"
                                                                                                                                                     1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV
                                                                                                                                                                                     HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYOSKVKRQIFSDYQSEVDIYNRIRDEL
                                                                                                                                                                                                ;;
 Length 380;
                         Indels
Score 1280; DB 22;
Pred. No. 1.6e-124;
L; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                      Plant-optimized E. coli LT-A A63K+R192G mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 |..ı>
/label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20..259
/label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BOYC-) BOYCE THOMPSON INST PLANT RES. MASO/) MASON H S.
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5; Page -; 103pp; English
                     1,
                                                                                                                                                                                                                                                                    AAY96650 standard; Protein; 259
 98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label- S63K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US30747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0113507
                                                                                                                                                                                                                                                                                                                 (first entry)
                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arntzen CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-442653/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211
             Similarity
                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200037609-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-DEC-1999;
                                                                                                                                                                                                                                                                                                                 26-SEP-2000
                         237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mason HS,
 Query Match
Best Local S:
Matches 237,
                                                                                                                                                                                                                                                                                          AAY96650;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ARNT/)
                                                                                                                                                                                    181
                                                                                                                                                                                                           197
                                                                                                                                                                                                                                                      AAY96650
                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
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This is Escherichia coli heat-labile toxin (LT) A subunit (LT-A) double mutant S63R-R192G. The wild-type serine was replaced with lysine at residue 63 and wild-type arguinne was replaced with lysine at residue 192 of the mature protein. The coding sequence contains plant preferred codons and eliminates sequence motifs associated with spurious mRNA processing. A single codon insertion (GTG encoding valine) was made to processing. A single codon insertion (GTG encoding valine) was made to accommodate the creation of a Ncol restriction site arcund the initiator methionine codon. Novel polynucleotides encode a mutant LT-A polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the prophylactic or therapeutic treatment against E. coli or V. cholerae. The mutant polypeptides are also useful as adjuvants for the prophylactic from the propertion of the specification. It was constructed from the wild type LT-A shown in AAY96646 which is given in Figure 1 of the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heat-labile toxin, LT-8, LT-B; mutant; transgenic plant; vaccine; oral; adjuvant; anti-bacterial; A72R+R192G; double mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 ngdklyradsrppdeikrsgglmprghneyfdrgtqmninlydhargtqfgfvryddgyv 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "the wild type alanine is replaced by glycine at position 72 of the mature sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1276; DB 21;
Pred. No. 2.4e-124;
4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant-optimized E. coli LT-A A72R+R192G mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20..259
/label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY96651 standard; Protein; 259 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.9%;
97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= R192G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 97.5
Matches 234; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 211
                                                                                                                                                                                                                                                                                                                                                                                                                       259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY96651;
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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This is Escherichia coll heat-labile toxin (LT) A subunit (LT-A) double mutant A72R-R192G. The wild-type alanine was replaced with arginine at residue 72 and wild-type arginine was replaced with alginine at residue 20 of the mature protein. The coding sequence contains plant-preferred codons and eliminates sequence motifs associated with spurious mRNA processing. A single codon insertion (GTG encoding valine) was made to processing. A single codon insertion (GTG encoding valine) was made to methionine codon. Novel polynucleotides encode a mutant LT-A polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A subunit (GT-A) polypeptide, which have reduced enzyme activity as compared to the vild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible
/note= "the wild type arginine is replaced by glycine
at position 192 of the mature sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccines, especially oral vaccines in transgenic plants for the prophylactic or therapeutic treatment against E. coli or V. cholerae. The mutant polypeptides are also useful as adjuvants. Note: This sequence does not appear in the specification. It was constructed from the wild type LT-A shown in AAY96646 which is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
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                                                                                                                                                                                                                                                                                                                                                      transformation of plant cells, useful in immunogenic compositions elicit immune responses in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .21 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.8%; Score 1275; DB 21;
97.5%; Pred. No. 3.1e-124;
iive 4; Mismatches 2;
                                                                                                                                                                                                                  (BOYC-) BOYCE THOMPSON INST PLANT RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 5; Page -; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in Figure 1 of the specification.
                                                                                                                                   99WO-US30747.
                                                                                                                                                                            98US-0113507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 97.5
Matches 234; Conservative
                                                                                                                                                                                                                                                                                           Mason HS, Arntzen CJ;
                                                                                                                                                                                                                                  (MASO/) MASON H S.
(ARNT/) ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                 WPI; 2000-442653/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 AA;
                                                        WO200037609-A2
                                                                                                                                   22-DEC-1999;
                                                                                                                                                                            22-DEC-1998;
                                                                                               29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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RESULT 13

AAW67772

g

237

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AAR38728 standard; Protein; 236

RESULT 14

AAR38728

E.coli heat labile toxin subunit A.

(first entry)

08-DEC-1993

AAR38728;

g

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121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI

61

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STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP

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the E. coli heat labile toxin, an example of a bacterial ADP-ribosylating toxin. A mutant detoxified form of this protein is used in a parenteral adjuvant composition, which comprises the detoxified protein, at least one selected antigen and optionally a pharmaceutically acceptable (optionally topical) vehicle. The adjuvant composition can be administered parenterally in conjunction with at least one antigen in methods to immunise vertebrate subjects. The adjuvant has the ability to enhance the humoral and cell-mediated immune responses elicited by the antigen (e.g. by making the antigen more strongly immunogenic or necessitating fewer/lower antigen doses). It can be administered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolation from antigens as a boost following systemic or mucosal antigen administration. Most preferably, the adjuvant is co-administered with the antigen in the compositions and a pharmaceutically acceptable carrier. The antigen may be derived from viruses, bacteria, parasites and fungi or may be tumour antigens, self-antigens and allergens. The compositions are therefore useful in the treatment and prevention of e.g. viral diseases, allergic manifestations, diseases caused by pathogens (e.g. bacteria or parasites), Albs, autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence corresponds to the amino acid sequence of the A subunit of
                                                                                                                                                         A subunit; heat labile toxin; ADP-ribosylation; mutant; detoxification; parenteral adjuvant; antigen; antigen; immunisation; humoral response; cell-mediated immune response; virus; bacterium; parasite; fungus; tumour; allergen; pathogen; ALDS; autoimmune disease; cancer; antibody; systemic lupus erythematosus; Alzheimer's disease; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prior/subsequent to the antigen, and is preferably administered within a short space of time to the same site; it can also be administered in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adjuvant can also be used to prepare antibodies against selected igen(s), useful e.g. for diagnostic purposes or for antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detgxified mutants of bacterial ADP-ribosylating toxins as parenteral adjuvants - useful to enhance humoral and cell-mediated immune responses in vertebrates when administered with selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rappuol1 R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 1A-B; 51pp; English.
  Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen e.g. in disease treatment
AAW67772 standard; Protein; 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Del Giudice G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0044696,
                                                                                                                                                                                                                                                                                                                                                                                                          98WO-0S05454
                                                                              (first entry)
                                                                                                                      E. coli heat labile toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-070064/06.
N-PSDB; AAV81595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 AA;
                                                                                                                                                                                                                                                                                      Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barchfeld G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigen(s), u
purification.
                                                                                                                                                                                                                                                                                                                            WO9842375-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-1997;
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                                                                              11-MAY-1999
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                                          AAW67772;
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This is the sequence of the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans. The sequence was published by Yamamoto et al., J.Biol. Chem., 259, 5037-5044. Mutations at selected positions within this sequence have been found to reduce toxicity (see AAR89730-R88732 and AAR44016-R44025). The invention relates to such immunogenic, detoxified proteins and their use in vaccines to protect against enterotoxigenic E.coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NGDRIKRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ngdrlyradsrppdeikrfrslmprg-neyfdrgtqmninlydhargtqtgfvryddgyv
                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic detoxified mutant cholera toxin and heat labile toxin - useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                      enterotoxigenic bacteria; vaccine; immunogenic detoxified LT-A; protomer A; site-directed mutagenesis; reduced toxicity; ADP-ribosyltransferase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1183; DB 14; Length 236;
Pred. No. 1e-114;
2; Mismatches 10; Indels 4
                                                                                                                                                                                                                                                                                                                                                         Rappuoli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 2; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                         Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.7%;
                                                                                                                                                                                                                                                              92WO-EP03016.
                                                                                                                                                                                                                                                                                           91IT-0MI3513
                                                                                                                                                                                                                                                                                                                          (BIOC-) BIOCINE SCLAVO SPA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 AA;
                                                                                                                                                                    Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ42768
                                                                                                                                                                                                                                                                                                                                                        Domenighini M,
                                                                                                                                                                                                                                                              30-DEC-1992;
                                                                                                                                                                                                                                                                                             31-DEC-1991;
                                                                                                                                                                                                  WO9313202-A.
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1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTOMNINLYDHARGTOTGFVRYDDGYV 60

91.3%; Score 1190.5; DB 20; Length 237; 92.9%; Pred. No. 1.7e-115;

Pred. No. 1.76 ; Mismatches

3;

Conservative

Similarity

Local Simi hes 223;

à

Ouery Match Best Loca Matches

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The present invention relates to peptides which exhibit anti-retroviral activity. The peptides of the invention (AAU1255-AAU14009) comprise DP178-like and DP107-like peptides. The DP178 peptide corresponds to amino acids 639-673 of the transmembrane protein gp41 from human immunodeficiency virus 1 (H1V-1) isolate LAI. The DP107 peptide corresponds to amino acids 558-595 of gp41 from HIV-LIAI. The invention also relates to a method of identifying compounds that inhibit the formation of identifying compounds that inhibit the formation of a DP107/DP178 complex. The method comprises detecting the formation of a DP107/DP178 complex, both in the presence or absence of a test compound, in a reaction mixture containing DP107. and DP178 peptides. The method is useful for identifying compounds, in a reaction mixture containing DP107. Including small molecule compounds, which may themselves exhibit antifusogenic, antiviral or intracellular modulatory activity. The DP178-like/DP107-like peptides are useful to inhibit human and non-human present sequence represents a peptide sequence from Escherichia coli heat labile enterotoxin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying a compound that inhibits the formation of or disrupts a DP107/DP178 complex, especially compounds with antifusogenic, antiviral or intracellular modulatory activity, by detecting the formation of a
                                                         180
                                                                                                                        Anti-retroviral; DP178-like; DP107-like; heat labile enterotoxin A;
                                                   121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI
                                                                                                                                                                                                                                                                                                                                                            Peptide sequence from Escherichia coli heat labile enterotoxin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Merutka G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lawless MK,
                                                                                                                                                                                                                                                                                                                                                                                                                 antifusogenic; antiviral; HIV transmission
                                                                                                                                                                                                                                                AAU14105 standard; peptide; 254 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Erickson JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 43; 259pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2000; 2000WO-US35727.
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                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TRIM-) TRIMERIS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
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Gaps

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Indels

90.7%; Score 1183; DB 22; 93.3%; Pred. No. 1.1e-114; ive 2; Mismatches 10;

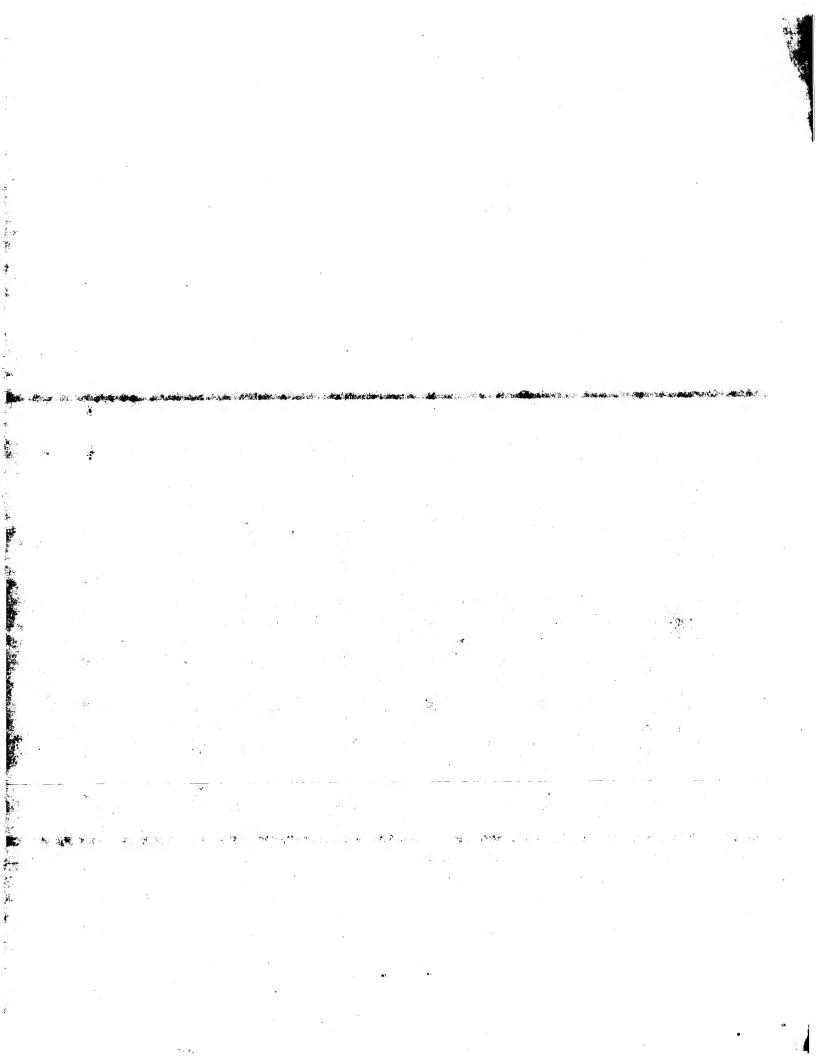
Similarity 93.3

Query Match Best Local Simi Matches 224;

Length 254;

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STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                              YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                  1 NGDALYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
          61
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Search completed: June 10, 2002, 17:31:46 Job time: 1053 sec



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June 10, 2002, 17:29:43 ; Search time 19.04 Seconds (without alignments) 1211.210 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                              OM protein - protein search, using sw model
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US-09-297-171-1 1304 1 NGDRLYRADSRPPDEIKRSG......QIFSDYQSEVDIYNRIRDEL 240 283138 seqs, 96089334 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table: Searched:

Total number of hits satisfying chosen parameters:

283138

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	labile ente	cholera enterotoxi	heat-labile entero	heat-labile entero	cholera enterotoxi	pertussis toxin ch		pertussis toxin ch	ש	hypothetical prote	arylphorin precurs	hypothetical prote	pertussis toxin ch	hypothetical prote	guanine nucleotide	hypothetical prote	beta-glucosidase,	probable glutamate	probable tRNA nucl	mosquitocidal toxi	prion protein - Ch	prion protein - go	hypothetical prote		Ω		3	6-phosphofructo-2-	outer membrane ush
SUMMARIES	ΔI	QLECA	XVVCA	A29831	A61345	S39239	B25973	WEBR11	WEBR1P	A47402	T01849	A61619	560935	A25973	T46366	T40574	G81094	A48860	A72616	E72563	S27514	A34759	B34759	F96903	T15789	JU0268	S74920	S77704	KIRTFB	D39142
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æ	Query	98.7	83.4	52.1	30.3	11.7	7.4	7.1		7.0	•		6.9		6.7			9.9		9.9	6.4	6.4	6.4	6.4	6.4	6.3	•	6.3	٠	6.2
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major prion proteinikB protein - Esc	LEF-6 OTIZ8 - BOMD hypothetical prote beta-N-acetylhexos	major prion PrP-Sc major prion PrP27- major prion protei	prion protein - gr hypothetical prote phytoene dehydroge	probable secreted 70.3K hypothetical enterotoxin A - Cl	SCF complex protei probable ribonucle
A54330 B38529	T41//3 E71704 S60137	UJHYIH A23545 S53629	S37137 S75251 S16250	AD0649 A86389 S10869	T43398 H72510
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30	3 3 5 4 3 5	35 36 37	338 409	4 4 4 4 3	44

## ALIGNMENTS

STSLSLRSAHLAGGSILSGYSTYXIXVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120

61

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1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60

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A.Title: Cloning of a gene (zot) encoding a new toxin produced by Vibrio cholerae.
A.Reference number: A43864, MUD: 92112300
A.Reference number: A43864
A.Status: preliminary
A.Accession: B43864
A.Status: preliminary
A.Molecule type: DNA
A.Redesidues: 1-6 (SAUA)
A.Kross-references: GB: M83563; NID: 9155314; PIDN: AAA27583.1; PID: 9155316
A.Note: sequence extracted from NCBI backbone (NCBIN: 77488, NCBIP: 77496)
B.Heidelberg, J.F.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers
I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A.Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A.Reference number: A82035; MUID: 20406833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: A82197
A;Status: preliminary
A;Molecule type: DNA
A;Rossreferences: GB:AE004224; GB:AE003852; NID:g9655952; PIDN:AAF94614.1; GSPDB:GN
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N'Alternate names: LT-IIa
C;Species: Escherichia coli
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C;Accession: A2981
C;Accession: A2981
R;Pickett, C.L.; Weinstein, D.L.; Holmes, R.K.
J. Bacteriol. 169, 5180-5187, 1987
A;Title: Genetics of type IIa heat-labile enterotoxin of Escherichia coli: operon fus
A;Reference number: A91849; MUID:88032841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  As Gene: VC1457
As Map position: 1
C; Complex: the cholera enterotoxin molecule contains three kinds of chains; an alpha c; the chomplex: the chomplex: the choice is a chain to cate noncovalently with the subunit B, an aggregate of five beta chains C; Function:
A; Description: the active component of the toxin that is primarily responsible for C; Superfamily: heat-labile enterotoxin chain A
C; Keywords: enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F.1-18/Domain: Signal sequence #status predicted <SIG>
F.19-212/Product: cholera enterotoxin alpha chain #status experimental <CTA>
F.213-258/Product: cholera enterotoxin gamma chain #status experimental <CTG>
F.217/Disulfide bonds: interchain (to alpha chain) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
                                                                                                       PIDN:CAA41590.1; PID:g48889 J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 258
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                                                            A; Residues: 1-258 <DAM>
A; Residues: 1-258 <DAM>
A; Cross-references: EmBL:X58785; NID:948888;
R; Baudry, B.; Fasano, A.; Ketley, J.; Kaper, Infect. Immun. 60, 428-434, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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A; Molecule type: DNA
A; Residues: 1-258 <MEK>
B; Residues: 1-258 <MEK>
B; Bams, E.; de Wolf, M.; Dierick, W.
Submitted to the EMBL Data Library, March 1991
A; Description: Correction of the cholera toxin nucleotide sequence of the Vibrio cholera
A; Reference number: $14623
A; Accession: $14623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cho
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A Residues: 19-36, "R', 38;213-232 < KLA>
B Youffy. L. K.; Peterson, J. W.; Rurosky, A.
J. Bold. Chem. 256, 1225-12256, 1981
A; Title: Covalent structure of the gamma chain of the A subunit of cholera toxin.
A; Reference number: A32298; MUID:82053094
A; Rolecule type: protein
A; Residues: 213-246, TD', 249-255, "N', 257-258 < DUZ>
B; Dams, E. de Wolf, M.; Dierick, W.
Biochim. Biophys. Acta 1090, 139-141, 1991
A; Reference number: S17665; MUID:91355224
A; Reference number: S17665; MUID:91355224
A; Status: preliminary
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A;Accession: A91268
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A; Residues: 37.38,'L',40-44,'SE'.47-49,'B',51-55,'B',57,'B',59-60,'B',62-66,'Z',68-72,
R; Duffy, L.K.; Peterson, J.W.; Kurosky, A.
FEBS Lett. 126, 187-190, 1981
A; Title: Isolation and characterization of a precursor form of the 'A' subunit of chol A; Reference number: A91286; MUID:81212799
A; Accession: A91286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Vibrio cholerae
C; Date: 06-Jul-1982 #sequence_revision 26-Jan-1996 #text_change 01-Sep-2000
C; Date: 06-Jul-1982 #sequence_revision 26-Jan-1996 #text_change 01-Sep-2000
C; Accession: A05129; S14623; S14625; A91268; A91268; A91746; A92298; S17665; B43864; R; Mekalanos, J.J.; Swartz, D.J.; Pearson, G.D.N.; Harford, N.; Groyne, F.; de Wilde, Nature 306, 551-557, 1983
A; Reference number: A93320; MUID: 84068199
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A; Residues: 19, 'N', 21-27 <DUF>
R; Klapper, D.G.; Finkelstein, R.A.; Capra, J.D.
Immunochemistry 13, 605-611, 1976
A; Title: Subunit structure and N-terminal amino acid sequence of the three chains of
A; Reference number: A91746; MUID: 76259136
                                                                                                                                            cholera enterotoxin chain A precursor VC1457 [validated] - Vibrio cholerae
    STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A: Experimental source: strain 2125
A: Accession: 814625
A: Status: preliminary
A: Nolecule type: DNA
A: Residuary
A: Resi
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                                                                                             YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI
                                                                                                                                                                                                                                                                               HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL
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A; Cross-references: EMBL:X58785; NID:948888; PIDN:CAA41590.1;
A; Experimental source: strain 569B
K; Lal, C.Y.; Cancedda, F.; Chang, D.
FEBS Lett. 100, 85-89, 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <DA1>
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cholera enterotoxin chain A2 - Vibrio cholerae (serotype 0139)
N;Alternate names: CTA2 cholera toxin chain A2
S;Species: Vibrio cholerae
A;Variety: serotype 0139
C;Date: 08-May-1995 **Sequence_revision 26-Jul-1996 **text_change 16-Jul-1999
C;Accession: S39239; S39240
R;Lebens, M.; Holmgren, J.
Submitted to the EMBL Data Library, November 1993
A;Description: Structure and arrangement of the Cholera toxin genes in vibrio Cholera A;Reference number: S39238
A;Reference number: S39238
A;Recsion: S39239
A;Molecule type: DNA
A;Residues: 1-46 <LEB>A;Ression: SEMBL:X76390; NID:9433856; PIDN:CAA53974.1; PID:9433858; EMBL:X763
A;Cross references: EMBL:X76393; Seperfamily: heat-labile enterotoxin chain A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pertussis toxin chain SI precursor - Bordetella parapertussis
C;Specias: Bordetella parapertussis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: B25973
F;Arico, B.; Rappuoli, R.
J. Bacteriol. 169, 2847-2853, 1987
A;Title: Bordetella parapertussis and Bordetella bronchiseptica contain transcription
A;Reference number: A25973; MUID:87222217
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 PDHQAWREEPWIHHAPQGCGNSSRT----ITGDTCNEETQNLSTIYLREYQSKVKRQIFS 224
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                                                                                                                                                                                                                                                                                                                                                                                                                             11.7%; Score 152; DB 2; Length 46
63.6%; Pred. No. 2.4e-07;
tive 9; Mismatches 7; Indels
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A; Residues: 1-269 <ARI>
C; Superfamily: pertussis
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C;Accession: A61345
K;Spicer, E.K.; Kavanaugh, W.M.; Dallas, W.S.; Falkow, S.; Konigsberg, W.H.; Schafer, D. Proc. Natl. Acad. Sci. U.S.A. 78, 50-44, 1981
A;Ittle: Sequence homologies between a subunits of Escherichia coll and Vibrio cholerae A;Reference number: A61345; MUID:81223767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G
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Note: authors translated the codon GAG for residue 27 as Asp, CAA for residue 53 as Superfamily: heat-labile enterotoxin chain A
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C;Species: Escherichia coli
C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPYSQIY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQ 185
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                                                                                                                                                                                                                                                                                                                                                         6 YRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSLS 65
                   A Molecule type: DNA
A; Residues: 1-259 <PIC>
A; Residues: 1-259 <PIC>
A; Cross-references: GB:M17894; NID:g146671; PIDN:AAA24093.1; PID:g146672
A; Cross-references: GB:M17894; NID:g146671; A; Note: the authors translated the codon TAT for residue 225.as Thr
C; Superfamily: heat-labile enterotoxin chain A
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-259/Product: heat-labile enterotoxin IIa chain A #status predicted <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 GCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQI-FSDYQSEVDI--YNRIRDEL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 QCVPNNKEFKGGVCISATNVLSKYDLANFKKLLKRRLALTFFMSEDDFIGVHGERDEL 259
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                                                                                                                                                                                                                                   52.1%; Score 679.5; DB 2; 54.6%; Pred. No. 8.2e-55; tive 39; Mismatches 66;
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Pred. No. 4.7e-29;
2; Mismatches 6;
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ilarity 39.9%;
Conservative 2
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30; Conservative
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Best Local Similarity
Matches 87; Conserv
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A;Molecule type: DNA
A;Residues: 1-125 <SPI>
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  A; Accession: A29831
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                                                                                                                                                                                                                                                              Best Local
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A; Molecule type: protein
A; Residues: 152-162, X²,164-166 <CCC>
A; Residues: 152-162, X²,264-166 <CCC>
A; Experimental source: strain 10536
C; Comment: See PIR:WEBR1 for version 1 of this sequence.
C; Superfamily: pertussis toxin chain S1
C; Superdiamily: pytosyltransferase; mitogen; pentosyltransferase; toxin; virulence factc—C; Reywords: glycosyltransferase; mitogen; pentosyltransferase; toxin; virulence factc—F; 13-34/Domain: signal sequence #status predicted <SIG>F; 35-269/Product: pertussis toxin chain S1 #status predicted <MAT>
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J. Biol. Chem. 268, 1765-17668, 1993
A;Title: Cloning of a rat adipocyte membrane protein implicated in binding or transpo-
A;Reference number: A47402; MUID:93352566
                                                                                                                                                                                                                       pertussis toxin b
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C; Superfamily: lysosomal integral membrane protein II
C; Keyvords: glycoprotein; transmembrane protein
F; 2-6/Domain: intracellular #status predicted <CYT1>
F; 7-30/Domain: intracellular #status predicted <TM1>
F; 7-30/Domain: extracellular #status predicted <TM1>
F; 749/Domain: extracellular #status predicted <TM2>
F; 740-466/Domain: intracellular #status predicted <TM2>
F; 740-00main: intracellular #status predicted <CYT2>
F; 75,102,134,205,220,235,247,417/Binding site: carbohydrate (Asn) (covalent) #status
                                              A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual A;Molecule type: DNA A;Residues: 35-64 <CIE>
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C;Date: 19-May-1995 #sequence_revision 12-Apr-1996 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 SLR-----SAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYE 110
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                                                                                                                                                                                         FEBS Lett. 249, 329-332, 1989
A;Title: Identification of an active-site residue in subunit S1 of
A;Reference number: S04494; MUID:89290006
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0.63;
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A; Reference number: A36176; MUID:88263009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
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Best Local Similarity 24.0%;
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Best Local Similarity
'Thes 56; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
                                 A; Accession: A36176
                                                                                                                                                                                                                                                                                             A; Accession: S04494
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                                                                                                                                                        R; Cockle, S.A.
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                                                                                                                                                                                                                                                                                                          A; Residues: 1-268 <LOC>
A; Residues: 1-268 <LOC>
A; Residues: 1-268 <LOC>
A; Cross-references: GB:M1323
C; Comment: Pertussis toxin contains five different chains, S1-S5. These are organized in c; Comment: Pertussis toxin contains of S2-S4 and S3-S4 are held together by S5. The genes C; Comment: Pertussis toxin causes irreversible uncoupling of the regulatory GTP-binding C; Comment: The substrates for the ADP-ribosyltransferase activity are the GTP-binding pt C; Comment: Pertussis toxin is the major virulence factor of B. pertussis.
C; Comment: See PIR:WBBRIP for version 2 of this sequence.
C; Superfamily: pertussis toxin chain S1
C; KGywords: glycosyltransferase; mitogen; pentosyltransferase; toxin; virulence factor; F; 1-34/Domain: signal sequence #status predicted <SIG>
F; 35-268/Product: pertussis toxin chain S1 #status predicted <MAT>
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R;Cleplak, W.; Burnette, W.N.; Mar, V.L.; Kaljot, K.T.; Morris, C.F.; Chen, K.K.; Sato, Proc. Natl. Acad. Sci. U.S.A. 85, 4667-4671, 1988
A;Title: Identification of a region in the S1 subunit of pertussis toxin that is require
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-269 <NIC>
A; Residues: 1-269 <NIC>
A; Cross-references: GB:M14378; NID:g144070; PIDN:AAA83980.1; PID:g144071
A; Cross-references: GB:M14378; NID:g144070; PIDN:AAA83980.1; PID:g144071
B; Loosmore, S.M.; Cunningham, J.D.; Bradley, W.R.; Yao, F.L.; Dekaban, G.A.; Klein, M.H.
Nucleic Acids Res. 17, 8365, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pertussis toxin chain S1 precursor (version 2) - Bordetella pertussis
N.Alternate names: histamine-sensitizing factor; islet-activating protein; lymphocytosis
N.Contains: NAD+ ADP-ribosyltransferase (EC 2.4.2.30)
C;Species: Bordetella pertussis
C;Date: 30-Sep-1997 #sequence_revision 30-Sep-1987 #text_change 24-Sep-1999
C;Accession: A24144; S06588; A36176; S04494
R;Nicosia, A.; Perugini, M.; Franzini, C.; Casagli, M.C.; Borri, M.G.; Antoni, G.; Almon Proc. Natl. Acad. Sci. US.A. 83, 4631-4635, 1986
A;Title: Cloning and sequencing of the pertussis toxin genes: operon structure and gene A;Reference number: A94104; MUID:86259651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                   C;Species: Bordetella pertussis
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 24-Sep-1999
C;Accession: A24399
R;Locht, C:, Keith, J.M.
Science 232, 1256-1264, 1986
A;Title: Pertussis toxin gene: nucleotide sequence and genetic organization.
A;Reference number: A94285; MUID:86208173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLR-----SAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 QEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLN--IAPAEDGYRLAGFP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----EYVDTYGDNAGRILAGA-----LATYQ 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 93; DB 1; Length 268; Pred. No. 0.63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDHQAWREEPWIHHAPQGCGNSSRT----ITGDTCNEETQN 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEYLAHRRIP-----PENIRRVTRVYHNGITGETTTTEYSN 197
N; Contains: NAD+ ADP-ribosyltransferase (EC 2.4.2.30)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.1%; Scc...
24.0%; Pred. No. c...
'... 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-67,'E',69-231,'V',233-269 <LOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53; Conservative
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                                                                                                                                                                                                                                                        A; Molecule type: DNA
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Best Local 9
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hypothetical protein YPL055c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein LPE17c
C;Specias: Saccharomyces cerevisiae
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999
C;Accession: S60935
R;Winnett, E.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Hall, J.; Storms, R. submitted to the EMBL Data Library, October 1995
A;Reference number: S60921
A;Reference number: S60935
A;Residues: 1-332 < WIN>
A;Residues: 1-332 < WIN>
A;Cross-references: EMBL:039205; NID:g1079672; PID:g1079687; GSPDB:GN00016; MIPS:YPLO
A; Cross-references: GB:M73793; NID:g159077; PIDN:AAA74229.1; PID:g159078
A; Note: in the authors' translation, residue 306-Leu is omitted, residue 317-Asn icconetics:
C; Genetics: 30/1; 74/3; 352/3; 410/2
A; Introns: 30/1; 74/3; 352/3; 410/2
A; Note: single copy gene
C; Superfamily: arylphorin
C; Superfamily: arylphorin
F; 1-16/Domain: signal sequence #status predicted <SIG>F; 11,481/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                             12;
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                                                                                                                                                                                                                                                                                                                                                                                                           54 RYDDG-YVSTSLSLRSAHLAGQSILS-----GYSTYYIYVIATAPNMFNVNDVLG---- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SGDNIN-DIOF 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 FVR-----YDDGYVSTS--LSLRSAHLAGQ---SILSGYSTYYIYVIATAPNMFNVNDVL 101
                                                                                                                                                                                                                                                                                                                                                                            5 LYRADSRPPDEIKRSGGLMPRGHN---EYFDRG------TQMNINLYDHARGTQTGFV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 SKDNAYYFYANYSGPLTYEDNENLLSYFIEDIGWNSYYYYFHNRFPFWENGEQLIGPLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 RRGEIYYYVYQKILARYYLERLANGLGEIP------RFNWLD------KYQTSYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 -----RNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQGCGNSSRTITGDTCNEETQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GDRLYRADSRPPDE-----IKRS----GGLMPRGHNEYFDRGTQMNINLYDHARGTQTG
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                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                       6.9%; Score 90.5; Di
20.4%; Pred. No. 3.8;
iive 37; Mismatches
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llarity 19.0%; Pred. No. 2.2;
Conservative 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 PLLSSYQLPFAQRNDDYYLA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 LSTIYLREYQSKVKRQIFSDYQSEVDIYN 234
                                                                                                                                                                                                                                                                  Query Match 6.3°
Best Local Similarity 20.4%
Matches 55; Conservative
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Best Local Similarity
Matches 60; Conserv
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A; Map position: 16L
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C;Species: Galleria mellonella (greater wax moth)
C;Date: 21-Jul-1995 #sequence_revision 11-Aug-1995 #text_change 24-Sep-1999
C;Accession: A61619
R;Memmel, N.A.; Trewitt, P.M.; Silhacek, D.L.; Kumaran, A.K.
R;Memmel, N.A.; Trewitt, P.M.; 331-342, 1992
A;Memmel, N.A.; Trewitt, P.M.; 331-342, 1992
A;Meference number: A61619
A;Reference number: A61619
A;Reference number: A61619
A;Reference per DNA
A;Residues: 1-702 <AMEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Typothetical protein F9D12.5 - Arabidopsis thaliana C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T01849
R;Murray, J.; Langston, Y.; Ahrens, C.
submitted to the EMBL Data Library, July 1998
A;Description: The Sequence of Arabidopsis thaliana F9D12.
A;Reference number: Z1444
A;Accession: T01849
A;Accession: Jaga cMUR>
A;Coss-references: EMBL:AF077407; NID:g3319339; PID:g3319347
C;Genetigs:
A;Map position: 4
A;Introns: 36/3; 134/2; 191/1; 283/2; 339/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                 ||: | |:| | : 226 | HEQTRSLKELLWGYKDPFLSLVPYPISTTVGVF--YPYNNTVDGVYKVSNGKDNISKVAI 226
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                                                                                                                                                                                                                                                  162 EYLPRGWEVNYDLKLFIH-NGKLNKYLAISDGTLKLYNDAKREWGFGQLIPHVTFYNTYG 220
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                                                                                                  --PHPYEQEVSALGGIPYSQ-IYGWYRVNFG-----V
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     YDDGYVSTSLSLRSAHLAGQSILSGYSTYY IYVIATAPNMFNVNDVLGVYS-
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Best Local Similarity 21.5%; Pred. No. 1.6;
Matches 45; Conservative 44; Mismatches
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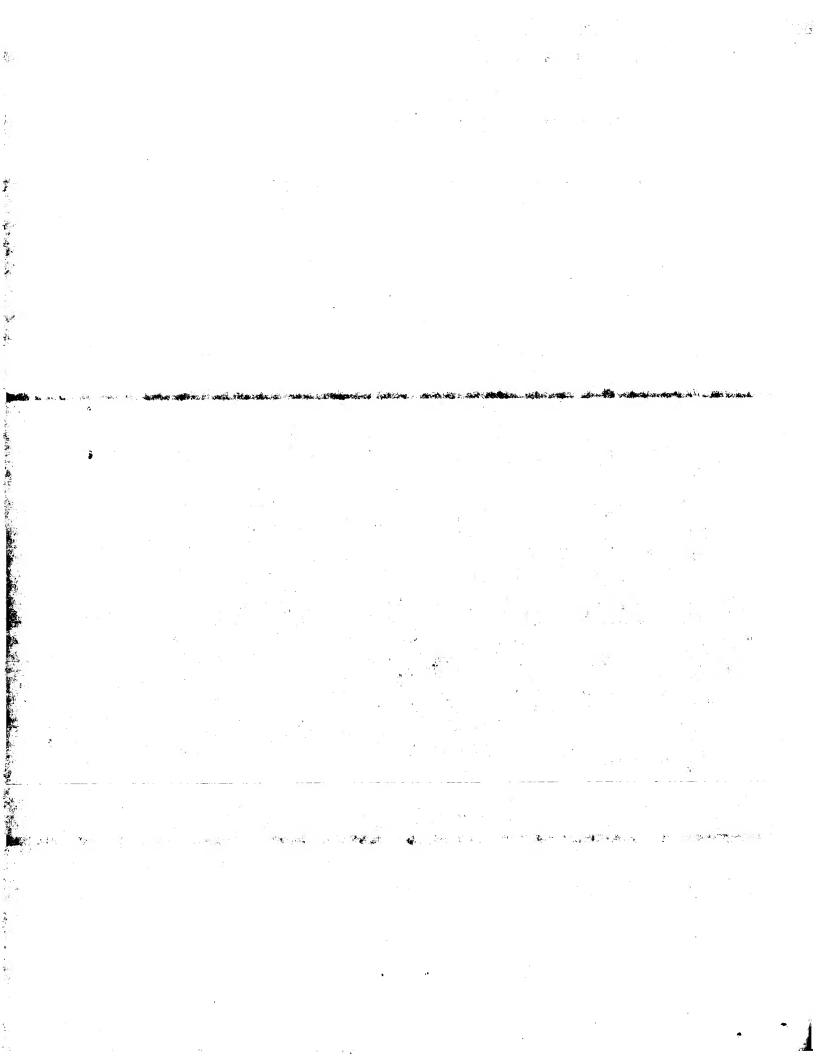
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guanine nucleotide binding protein beta subunit-like - fission yeast (Schizosaccharom
                                                                                                                                                                                                                                                                                                                       C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40574
R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 1999
A;Reference number: 221938
A;Reference number: 221938
    ---FGVIDERL-HRNREYRDRYYRNL 153
                                                                                              415 EEPQSIVPRLRTRNTRTDAILLGHYRLSQDTDNQTKVFAVITKKKEEKPLDYKYRYFRRV 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NGD---RLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDD 57
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-809 <SEE>
A;Cross-references: EMBL:AL035226; PIDN:CAA22832.1; GSPDB:GN00067
A;Experimental source: strain 972h-; cosmid c609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 809;
                                                                                                                                                     NIAPAEDGYR--LAGFPPDHQAWREEPWIHHAPQGCGNSSRTITGDT 198
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Job time: 169 sec
                                                                   HPYEQEVSAL - - - GGIPYSQIYGWYRVN - - -
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A;Introns: 21/1; 52/2; 280/3; 780/2
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246 CRCVRKFSPD 255
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Best Local Similarity
Matches 43; Conserv
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C.Species: Bordetella bronchiseptica
C.Species: Bordetella bronchiseptica
C.Species: Bordetella bronchiseptica
C.Accession: A25973
R.Arico, B.; Rappuoli, R.
A.Title: Bordetella parapertussis and Bordetella bronchiseptica contain transcriptionall
A.Roccession: A25973
A.Status: preliminary
A.Status: preliminary
A.Status: preliminary
A.Status: preliminary
A.Rosidues: 1-269 <ARI>
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C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T46566
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
A;Reference number: 223031
                                                                        223 V------HVPENRSNSDGSSSSVKKKRILDMKDSPFIYLTDFDKNVKKTNNTE 270
  --SSSHTYNNYHHRETPPPPSNGYYAKGYP 222
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                                         PDHQAWREEPWIHHAPQGCGN ... - SSRTITGDTCNEETQNLSTIYLREYQSKVK -
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A; Note: DKFZp434C0118.1
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23.4%; Pred. No. 4.7;
tive 32; Mismatches
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A;Molecule type: mRNA
A;Residues: 1-547 <AAA>
A;Cross-references: EMBL:AL137520
175 PSVSSITNNRSYHSSAYPY-
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271 SECEKAREVFKESDS 285
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  mycoplasma
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STRAIN-ISOLATE P307;
MEDLINE-82167425; PubMed-6279611;
Spicer E.K., Noble J.A.;
"Escherichia coli heat-labile enterotoxin. Nucleotide sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STARAIN-ISOLATE PS02;
MEDLINE-87137303; PubMed-3546573;
Yamamoto T., Gojobori T., Yokota T.;
FavOlutionary origin of pathogenic determinants in enterotoxigenic Escherichia coli and Vibrio cholerae 01.";
J. Bacteriol. 169:1352-1357(1987).
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STRAIN-ISOLATE P307;
Dykes C.W., Halliday I.J., Hobden A.N., Read M.J., Harford S.;
Dykes C.W., and the nucleotide sequence of the A subunit of heat-labile enterotoxin and cholera toxin.";
FEMS Microbiol. Lett. 26:171-174(1985).
                                                                                                                                                                                                                                                                                                               01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Heat-labile enterotoxin A chain precursor (LT-A, porcine) (LTP-A).
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MPLINE-3340541; Pubmed-8478941.
Sixma T.K., van Zanten B.A.M., Dauter Z., Hol W.G.J.;
"Refined structure of Escherichia coli heat-labile enterotoxin, close relative of cholera toxin.";
J. Mol. Biol. 230:890-918(1993).
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P20796 1
P51146 2
P52113 0
P4785 0
P4085 0
P41432 0
P6218 1
P16118 1
P13242 1
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P18142 0
P16118 1
P13242 1
P18136 1
P18136 1
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Trachman J.D., Maas W.K.;
Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                  ALIGNMENTS
             PRIO_ATEPA
PRIO_CAPHI
PRIO_ODOHE
PRIO_MUSVI
Y028_NPVAC
                                                                                                F261_HUMAN
PYRG_BACSU
SYQ_VIBCH
COE2_MOUSE
MBHL_RHILV
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J. Biol. Chem. 257:5716-5721(1982)
[4]
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MEDLINE=91093102; PubMed=2266142;
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  ELTA OR LTPA.
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1 NGDRLYRADSRPPDEIKRSG.....QIFSDYQSEVDIYNRIRDEL
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- 2000 Compugen Ltd
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CHTA_VIBCH
E2BA_ECOLI
E2AA_ECOLI
TOXI_BORPE
CD36_RAT
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FBX9_HUMAN
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PRIO_CRIGR
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Y455_RICPR
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PRIO_CEREL
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Gapop 10.0 , Gapext 0.5
              GenCore
Copyright (c) 1993
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length: 2000000000
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                                                                     'Crystal structure of a cholera toxin-related heat-labile enterotoxin
                MEDLINE=91238966; PubMed=2034287;
Sixma T.K., Pronk S.E., Kalk K.H., Wartna E.S., van Zanten B.A.M.,
Witholt B., Hol W.G.J.;
                                                                                                                                     DISCUSSION OF SEQUENCE.

MEDLINE=95349400; PubMed=7623669;
Domenighini M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli R.;
Domenification of errors among database sequence entries and comparison of correct amino acid sequences for the heat-labile enterotoxins of Escherichia coli and Vibrio cholerae.";
MOI MICTOBIOL 15:1165-1167(1959).

THE A CHAIN, WHICH ACTIVATES INTRACELLUIAR ADENYL CYCLASE.

SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
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SGG -> FRS (IN REF. 3).
MISSING (IN REF. 3).
S -> Y (IN REF. 3).
TYYIYUTATAP -> LITIVIJA (IN
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R -> G (IN REF. 4).
N -> D (IN REF. 3).
X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
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                                                                                                    Nature 351:371-377(1991).
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PDB; ILTB; 31-JAN-94.
PDB; ILTG; 15-SEP-95.
PDB; ILTT; 17-AGG-96.
PDB; ILTT; 31-JAN-94.
PDB; ILTT; 31-JAN-94.
PDB; ILTT; 31-JAN-94.
PDB; ILTT; 20-JAN-97.
PDB; ILTT; 16-JAN-97.
                                                                                       from E. coli."
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Yamamoto T., Tamura T., Yokota T., "Primary structure of heat-labile enterotoxin produced by Escherichia coli pathogenic for humans.";
J. Biol. Chem. 259:5037-5044(1984).
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943530,
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
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STRAIN=ISOLATE H10407;
MEDLINE=84185610; PubMed=6325417;
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196
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Query Match
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SEQUENCE OF 1-212 FROM N.A.
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STRAIN-1854 / Ol39-BENGAL;
                                                                                                                                                                                                                                                                                            vaccine development.";
Nature 306:551-557(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                         strain 569B.
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                                                                                                                           Vibrio cholerae
                                                                                                                                                               NCBI_TaxID=666;
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                                                                                                                                                                                                                                                             de Wilde M.;
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                                                                                                          SEQUENCE FROM N.A.
STRAIN-ISOLATE H10407;
STRAIN-ISOLATE H10407;
MEDILINE-9125225; Pubbed-8486242;
Inoue T., Tsuji T., Koto M., Imamura S., Miyama A.;
"Amino acid sequence of heat-labile enterotoxin from chicken enterotoxigenic Escherichia coli is identical to that of human strain H 10407.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
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          MEDIJNE-87137303; PubMed-3546273;
Yamamoto T., Gojobori T., Yokota T.;
Yamamoto T., Gojobori T., Yokota T.;
Escolutionary origin of pathogenic determinants in enterotoxigenic Escherichia coll and Vibrio cholerae Ol.";
J. Bacteriol. 169:1352-1357(1987).
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                                                                                                                                                                                                                                                                                          Rappuoli R.;
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-I. FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED ITHE A CHAIN, WHICH ACTIVATES INTRACELIULAR ADENYL CYCLASE.

-I. SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
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HEAT-LABILE ENTEROTOXIN A CHAIN.
BY SIMILARITY.
SIMILARITY.
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2BB153C777FD78B7 CRC64;
                                                                                                                                                                                                                          FEMS Microbiol. Lett. 108:157-161(1993)
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                                                                                                                                                                                                                                                       DISCUSSION OF SEQUENCE.
MEDLINE-95349400; PubMed-7623669;
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PRINTS; PR00771; ENTEROTOXINA.
Enterotoxin; Signal.
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Matches 237; Conservative
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RESULT

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SEQUENCE FROM N.A.
STRAIN-EL TOR N16961 / SEROTYPE 01;
MEDLINE-20406833; PubMed-10952301;
MEDLINE-20406833; PubMed-10952301;
Meddlaberg J.F., Eisen J.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CLASSIFAL 59B / ATCC 25870 / SEROTYPE 01;
MEDLINE-9135524; Pubbed-1883840;
Dams E., de Wolf M., Dierick W.;
"Nucleotide sequence analysis of the CT operon of the Vibrio cholerae
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CHTA_VIBCH STANDARD; PRT; 258 AA.

901555; Q019V1;
21-JUL-1986 (Rel. 01, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
1-OCT-2001 (Rel. 40, Last annotation update)
1-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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STRALM-EL TOR 2125;
Dams E., de Wolf M., Derick W.;
Submitted (MAY-1991) to the EMBL/GenBank/DDBJ databases.
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MEDLINE-85006737; PubMed-6090390;
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STRAIN-EL TOR 2125;
MEDLINE-84068199; Pubmed-6646234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95387395; PubMed=7658473; Zhang R.G., Scott D.L., Westbrook M.L., Nance S., Spangler B.D., Scott D.L., Westbrook E.M., Shipley G.G., Westbrook E.M., "The three-dimensional crystal structure of cholera toxin."; J.Mol. Biol. 251:563-573(1995).
-!- FUNCTION: THE ALPHA/GAWMA CHAIN (A SUBUNIT) IS AN ADP-RIBOSYLATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: NAD(+) + peptide diphthamide = nicotinamide + peptide N-(ADP-D-ribosyl)diphthamide.
SUBUNIT: CONTAINS 3 KINDS OF CHARNS. AN ALPHA AND A GAWMA CHAIN (FROM THE SAME PRECURES), LINKED BY AN INTERCHAIN DISULFIDE BOND, ASSOCIATE NONCOVALENTLY WITH AN AGGREGATE OF 4 TO
                                                                                                                                                                                                                                                                                                                                               Klapper D.G., Finkelstein R.A., Capra J.D.; "Subunit structure and N-terminal amino acid sequence of the three chains of cholera enterotoxin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lai C.-Y., Cancedda F., Chang D., Primary Structure of cholera toxin subunit Al: isolation, partial sequences and allgnment of the BrCN fragments."; FEBS Lett. 100:85-89(1979).
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Duffy L.K., Peterson J.W., Kurosky A.;
"Covalent structure of the gamma chain of the A subunit of cholera
"Nucleotide sequence analysis of the A2 and B subunits of Vibrio
                                                                                                                                                        Duffy L.K., Peterson J.W., Kurosky A.;
"Isolation and characterization of a precursor form of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
                                                    Biol. Chem. 258:13722-13726(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 256:12252-12256(1981).
                                                                                                                                        MEDLINE=81212799; PubMed=7238869;
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                                                                                                                                                                                                                                                                                                SEQUENCE OF 19-38 AND 213-232
                                                                                                                                                                                                             subunit of cholera toxin.";
FEBS Lett. 126:187-190(1981).
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EMBL, D30053, BAA06290.1,
EMBL, X58786, CAA41592.1,
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                              cholerae enterotoxin.
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                                                                                                      SEQUENCE OF 19-27
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TIGR; VC1457; -. InterPro; IPR001144; Enterotoxin\_A.

S14625; S14625. S17665; S17665. S14623; S14623. IXPB; 01-APR-97. IXTC; 01-AUG-96.

PIR;

A01818; XVVCA. A05129; A05129.

; K02679; AAA27514 11; AR175708; AAD51359 11; AE004224; AAF94614 11; CK01170; AAA06288 11; CH030052; BAA06288 11; CH030052; CH

EMBL; EMBL; EMBL; PIR; P

EMBL;

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YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
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MEDLINE=96399713; PubMed=8805549;
Van den Akker F., Sarfaty S., Twiddy E.M., Connell T.D., Holmes R.K.,
Hol W.G.J.;
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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STRAIN=ISOLATE 41;
MEDLINE=89359131; Pubmed=2670900;
Pickett C.L., Twiddy E.M., Coker C., Holmes R.K.;
Pickett oll., Twiddy E.M., Coker C., Holmes R.K.;
IIb heat-labile enterotoxin gene of Escherichia coll.";
J. Bacteriol. 171:4945-4952(1989).
                                                                            CHOLERA ENTEROTOXIN, CHAIN-A1 (ALPHA).
CHOLERA ENTEROTOXIN, CHAIN-A2 (GAMMA).
INTERCHAIN (WITH GAMMA CHAIN).
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                                                                                                                            INTERACT WITH NAD (BY SIMILARITY).
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-!- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
-!- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Crystal structure of a new heat-labile enterotoxin, LT-IIb.";
                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 258;
           PRINTS; PR00771; ENTEROTOXINA. Transferase; Glycosyltransferase; 3D-structure; Complete proteome. SIGNAL SIGNAL
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01-NOV-1995 (Rel. 32, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
Heat-labile enterotoxin IIB, A chain precursor (LT-IIB).
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                                                                                                                                     BY SIMILARITY.

D -> N (IN REF. 9).

S -> R (IN REF. 10).

G -> L (IN REF. 11).

QS -> SE (IN REF. 11).

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S -> A (IN REF. 11).

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DI -> ID (IN REF. 12).

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D -> N (IN REF. 12).
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81.7%; Pred. No. 1e-9
ive 24; Mismatches
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Pfam; PF01375; Enterotoxin_A; 1.
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130
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111
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P43528;
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Best Local 9
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NCBI_TaxID=520;
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P04977;
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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Escherichia.
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                                                                                                                                                                                                                                   29485 MW; A56E8A069427CFB9 CRC64;
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01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
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PDB; 1TT1; PRELIMINARY.
InterPro; IPR001144; Enterotoxin_A.
Pfam; PP01375; Enterotoxin_A: I.
PRINTS; PR00771; ENTEROTOXINA.
Enterotoxin; Signal; 3D-structure.
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13-AUG-1987 (Rel. 05, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC toxin subunit 1 precursor (PTX S1) (Islet-activating protein S1) (IAP S1) (NAD-dependent ADP-ribosyltransferase (EC 2.4.2.-)).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 GWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 LRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPYSQIY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Loosmore S.M., Cunningham J.D., Bradley W.R., Yao E.L., Dekaban G.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 YRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSLS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 GCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQI-FSDYQSEVDI--YNRIRDEL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 QCVPNNKEFKGGVCISATNVLSKYDLMNFKKLLKRRLATFFMSEDDFIGVHGERDEL 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 FRADSRIPDEIRRAGGLLPRGOOEAYERGTPININLYEHARGTVIGNTRYNDGYVSTIVT
                                                                                                                                                                                                                   HEAT-LABILE ENTEROTOXIN IIA, A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDILINE-86259651; PubMed-2873570; Nicosia A., Perugini M., Franzini C., Casagli M.C., Borri M.G., Antoni G., Almoni M., Neri P., Ratti G., Rappuoli R.; "Cloning and sequencing of the pertussis toxin genes: operon structure and gene duplication.";
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                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      66; Indels
                                                                                                                                                                                                                                      SIMILARITY.

SIMILARITY.

996F311A32CABEAA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                           52.1%; Score 679.5; DB 1
54.6%; Pred. No. 3.2e-55;
iive 39; Mismatches 66
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                                                                      InterPro; IPR001144; Enterotoxin_A. Pfam; PF01375; Enterotoxin_A; 1. PRINTS; PR00771; ENTEROTOXINA. Enterctoxin; Signal. 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-90045957; PubMed-2554254;
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EMBL; M17894; AAA24093.1;
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215
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                            PIR; A29831; A29831.
HSSP; P43528; 1TII.
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128
128
259 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sensor.;

J. Mol. Biol. 258:661-671(1996).

- FUNCTION: SI IS AN NAL-DEPENDENT ADP-RIBOSYLTRANSPERASE. IT
CATALYZES THE ADP-RIBOSYLATION OF A CYSTEINE IN THE ALPHA SUBUNIT
OF HETEROTRIMERIC G PROTEINS. IN THE ABSENCE OF G PROTEINS IT ALSO
CATALYZES THE CLEAVAGE OF NAD(+) INTO ADP-RIBOSE AND NICOTINAMIDE.

IT IRREVERSIBLY UNCOUPLES THE G-ALPHA GTP-BINDING PROTEINS FROM
THEIR MEMBRANE RECEPTORS.

- SUBUNIT: PERTUSSIS TOXIN CONTAINS FIVE DIFFERENT CHAINS, S1-S5.

THEY ARE ORGANIZED INTO 2 FUNCTIONAL SUBUNITS: A, COMPOSED OF SI
(WHICH IS TOXIC) AND E, CONTAINING S2, S3, S5, AND TWO COPIES OF
S4 (B BINDS TO THE MEMBRANE RECEPTORS). DIMERS OF S2-S4 AND S3-S4
ARE HELD TOGETHER BY S5.
                                          Cockle S.A.; "Identification of an active-site residue in subunit S1 of pertussis
                                                                                                                                                                                                                                                                                                                                                                                          proposed mechanism of ADP-ribosylation catalyzed by the pertussis
                                                                                                                                                                    the S-1
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MEDLINE-SC19180, PubMed-e6637000;
Hazes B., Boodhoo A., Cockle S.A., Read R.J.;
"Crystal structure of the pertussis toxin-ATP complex: a molecular
                                                                                                                                                                                                                                                                    Rappuoli R.;
"Further analysis of the sequence of the S1 subunit of pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S.A., Klein M.H.
                                                                                                                                               Cortina G., Barbieri J.T.;
"Role of tryptophan 26 in the NAD glycohydrolase reaction of
                                                                                                                                                                                                                                                         Pizza M., Bugnoli M., Puccini P., Siciliano R., Marino G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94356444; PubMed-8075982;
Stein P.E., Boodhoo A., Armstrong G.D., Cockle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The crystal structure of pertussis toxin."; Structure 2:45-57(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
                                                                                                                                                                                ounit of pertussis toxin.";
Biol. Chem. 264:17322-17328(1989).
                                                                                                                                                                                                                                                                                                                                                ACTIVE SITE, AND CATALYTIC MECHANISM.
               AND SEQUENCE OF 153-169
                                                                        toxin by photocrosslinking to NAD. FEBS Lett. 249:329-332(1989).
                                                                                                                                                                                                                                                                                                                   Infect. Immun. 59:1177-1179(1991).
                                                                                                                                                                                                                         CHARACTERIZATION.
MEDLINE-91147200; PubMed-1997420;
[4]
ACTIVE SITE, AND SEQUENCE OF 153-
MEDLINE=89290006; PubMed=2737291;
                                                                                                                                    MEDLINE-90008894; PubMed-2551899;
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EMBL; X16347; CAA34397.1; -.
EMBL; M13223; AAA22981.1; -.
EMBL; A13359; CAA01091.1; -.
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                                                                                                                      TRYPTOPHAN 60.
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PIR; A24394; WEBRI.
PIR; S06588; S06588; PDB; 1PRT; 26-JAN-95.
PDB; 1BCP; 05-JUN-97.
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                                                                                                                              INTERACT WITH NOD.

INCREASE THE NUCLEOPHILICITY OF THE INCREASE THE NUCLEOPHILICITY OF THE WATER MOLECULE TO ATTACK THE WEAKENED N-GLYCOSIDIC BOND OF NAD(+) AND YIELD THE PRODUCTS OF THE REACTION.

EXERTS ITS ACTION ON THE 2'-OH GROUP OF THE NAD(+) RIBOSE, THERREY FACILIATING THE PORMATION OF AN OXCCARBONIUM-LIKE INTERMEDIATE AND THE WEAKENING OF THE N-
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01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Platelet glycoprotein IV (GPIV) (GPIIIB) (CD36 antigen) (PAS IV) (PAS-4 protein) (Fatty acid transport protein) (Fatty acid transport protein) (Fatty acid transport protein)
InterPro; IPR003898; Borpert_toxA.
Pfam; PF02917; Pertussis_S1; 1.
PRIMUS; PR01395; BORPETOXINA.
Toxin; Signal; Transferase; Glycosyltransferase; NAD; Whooping cough;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Adipocyte;
MEDLINE-93352566; PubMed-7688729;
Abumrad N.A., El-Maghrabi M.R., Amri E.Z., Lopez E., Grimaldi P.A.;
Abumrad N.A., El-Maghrabi M.R., Amri E.Z., Lopez E., Grimaldi P.A.;
"Cloning of a rat adipocyte membrane protein implicated in binding or transport of long-chain fatty acids that is induced during preadipocyte differentiation. Homology with human CD36.";
J. Biol. Chem. 268:17668-17668(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 SLR-----SAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 QEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLN--IAPAEDGYRLAGFP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------YGAASSYF-----EYVDTYGDNAGRILAGA----LATYQ 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62; Indels 84; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSL 64
                                                                                                                                                                                                                                                                                                                                                          D -> E (IN STRAIN 10536).
I -> V (IN STRAIN 10536).
RMAPUTG -> HGRGDS (IN REF. 3).
FGC88C16DAGE008AB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 SEYLAHRRIP----PENIRRVTRVYHNGITGETTTTEYSN 197
                                                                                                                                                                                                                                                                                                                         GLYCOSIDIC BOND.
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                                                                                                                  PERTUSSIS
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68
232
227
269 AA;
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35
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69
                                                                          3D-structure.
SIGNAL
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Best Local Simi:
Matches 53; (
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12;

Gaps

66

134

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Zea mays (Maize).
Eukaryophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                    55 YDDGYVSTSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYS----- 105
                                                                                                                                                                                                                                                                                                                                                                       MFQTRSLKELLWGYKDPFLSLVPYPISTTVGVF--YPYNNTVDGVYKVSNGKDNISKVAI 225
                                                                                                                                                                                                                                                                                                                                                                                                     135 IDE-RLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQGCGNSSRT 193
                                                                                                                                                                                                                  GDRLYRA----DSRPPDEIKRSGG---LMPRGHNEYFDRGTQMNINLYDHARGTQTGFVR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 34, Last annotation update)
Beta-glucosidase, chloroplast precursor (EC 3.2.1.21) (Gentiobiase)
(Cellobiase) (Beta-D-glucoside glucohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brzobohaty B., Moore I., Kristoffersen P., Bako L., Campos N., Schell J., Palme K.; "Release of active cytokinin by a beta-glucosidase localized to the
                                                                                                                                                                                                                                                                                                         116 PNCAIFEPSLSVGTE-----NDNFTVLNLAVAAAPHIYTNSFVQGVLNSLIKKSKSS
                                                                                                                                                                                                                                                                                                                                         Esen A.; "Purification and partial characterization of Maize (Zea Mays L.)
                                                                                                                                                      7.0%; Score 91.5; DB 1; Length 471; 80.1%; Pred. No. 0.65; ve 39; Mismatches 85; Indels 99
 I -> K (IN REF. 2).
S -> F (IN REF. 2).
LG -> FV (IN REF. 2).
R -> Q (IN REF. 2).
N -> I (IN REF. 2).
T -> N (IN REF. 2).
T -> N (IN REF. 2).
S -> A (IN REF. 2).
W; D344B567CB36ID77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRALM-CV. INBRED LINE K55; TISSUE-Shoot;
Esen A., Shahid M.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                  IDTYKGKRNLSYWESYCDMIN-----GTDAASFPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 ITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 55-69; 165-174; 207-213 AND 217-235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. MUTIN; TISSUE-Coleoptile; MEDLINE-94053747; Pubmed-8235622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Physiol. 98:174-182(1992)
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                                                                                                          52466
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Best Local Similarity 20.1%
Matches 56; Conservative
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SEQUENCE
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BGLC_MAIZE
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                                                                                                                                                                                                                                                                     Harmon C.M., Abunrad N.A.;

"Binding of Sulfosuccinimidyl fatty acids to adipocyte membrane proteins: isolation and amino-terminal sequence of an 88-kb protein implicated in transport of long-chain fatty acids.";

J. Membr. Biol. 133:49(1993).

-I-FUNCTION: SEEMS TO HAVE NUMBROSPONDIN, ANYONIC PHOSPHOLIPIDS AND OXIDIZED LDL. MAY FUNCTION AS A CELL ADHESION MOLECULE. DIRECTLY MEDIATES. CYTOADHERRUGE OF PLASMODIUM FALCIPARUM PARASITIZED BRYTHROCYPES. BINDS LONG CHAIN FATTY ACIDS AND MAY FUNCTION IN THE TRANSPORT AND/OR AS A REGULATOR AND ANY FUNCTION AND ACIDS AND MAY FUNCTION.
                                 by type
                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- TISSUE SPECIFILY: PREDMINANT IN HEART, INTESTINE, SPLEEN, FAT,
-SKELETAL MUSCLE, LOWER IN TESTES.
-1- DEVELOPMENTAL STAGE: INDUCED DURING PREADIPOCYTE DIFFERENTIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                 Guthmann F., Haupt R., Looman A.C., Spener F., Ruestow B.; "Fatty acid translocase/CD36 mediates the uptake of palmitate
                                                                                                                                   Jochen A., Hays J.;
"Purification of the major substrate for palmitoylation in
adipocytes: N-terminal homology with CD36 and evidence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PALMITATE (PROBBALE).
PALMITATE (PROBBALE).
PALMITATE (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
                                                         Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
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(GLCNAC...)
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N-LINKED (GLCNAC.)

N-LINKED (GLCNAC.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE CD36 FAMILY.
                                                                                                                                                                                                                                             STRAIN-SPRAGUE-DAWLEY; TISSUE-Adipocyte;
MEDLINE-93308714; Pubmed-8320718;
                                                                                          SEQUENCE OF 1-30, AND PALMITOYLATION.
                                                                                                        TISSUE-Adipocyte;
MEDLINE-94065506; Pubmed-7504047;
                                                                                                                                                                                            Lipid Res. 34:1783-1792(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor; Palmitate; Lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, L19658; AAA02878.1; -.
EMBL, AR072411; -.
InterPro; IPR001159; CD36.
Pfam: PF01130; CD36; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
438
460
471
                                                                                                                                                                                 surface acylation."
                                                                                                                                                                                                                                 SEQUENCE OF 1-15.
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78
101
STRAIN-WISTAR;
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TRANSMEM
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                                                                        THE MALLE LAW LIMENSEAURS OF PROPERTY OF THE MALLE OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                   Touzet P., Riccardi F., Mcrin C., Damerval C., Huet J.-C.,
Pernollet J.-C., Zivy M., de Vienne D.;
"The maize two dimensional gel protein database: towards an integrated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPGLDCAYPTGNSLVEPYTAGHNILLAHA-----EAVDLYNKH-YKRDDTRIGLAFDV 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------PPDHQAWREEP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 WIHHAPQGC-----GNSSRTIT----GDTCNEETQNLSTIYLREYQ--SKVKRQ 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 KRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSLS------ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| :| | : | | 317 MGRVPYGTSFLDKQAEERSWDINLGWFLEPVVRGDYPFSMRSLARERLPFFKDEQKEKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377 GSYNMLGLNYYTSRFSKNID: SPNYSPVLNTDDAYASQEVNGPDGKPIGPP-----MGNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52; Mismatches 101; Indels 109;
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NUCLEOPHILE (BY SIMILARITY).

A -> D (IN REF. 2).

E -> Q (IN REF. 2).

T -> A (IN REF. 2).

3, 4EA241258AE3641B CRC64;
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InterPro; IPR001360; Glycc_hydro_1.
InterPro; IPR001360; Glycc_hydro_1.
Pfan; PF00232; Glyco_hydro_1; 1.
PRINTS; PR00131; GLYCDKLASE1.
PR0SITE; PS00572; GLYCOSYL_HYDROL_F1_1; 1.
PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
Hydrolase; Glycosidase; Chloroplast; Transit peptide.
54 CHLOROPLAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 LGGIPYSQIY------GWY-----RVNFGVIDERLHRNR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 6.8%; Score 88.5; Similarity 17.1%; Pred. No. 1.5
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Maize-2DPAGE; P49235; COLEOPTILE.
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554 T
64237 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U25157; AAA65946.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X74217; CAA52293.1;
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554
566 AA;
TISSUE=Coleoptile;
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ACT_SITE
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tubby B.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Probably recognizes and binds to some phosphorylated proteins and promotes their ubiquitination and degradation.
-!- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX (BY SIMILARITY).
53 VRYDDGYVSTSLSLRSAHLAGQSILSGY-----STYYIYVIATAPNMFNVNDVLGVYSP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 121-447 FROM N.A.
MEDLINE-20003060; PubMed-10531035;
Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Elledge S.J., Harper J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.7%; Score 88; DB 1; Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification of a family of human F-box proteins."; Curr. Biol. 9:1177-1179(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             447 AA; 52329 MW; 2A88163DAB898D69 CRC64;
                                                                                                                                                                                                                                                                                 FBX9_HUMAN STANDARD; PRT; 447 AA. 090K97; 075986; CCT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Fbx09 OR FBX9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: CONTAINS 1 TPR REPEAT.
-!- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20003061; PubMed=10531037; Winston J.T., Koepp D.M., Zhu C., Elledd: "A family of mammalian F-box proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jbiquitin conjugation; TPR repeat. REPEAT 127 TPR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Curr. Biol. 9:1180-1182(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 121-447 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001810; F-box.
InterPro; IPR001440; TPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50181; FBOX; 1
                                                                                                                      492 I-ATLKESIDLGSNVQ 506
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Pfam; PF00515; TPR; 1.
                                                                                   222 IFSDYQSEVDIYNRIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pagano M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                              RESULT 9
FBX9_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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OF THE SPORE COAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                       154 DPQVMSW 160
                                                                                                             168 PPDHQAW 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-TERMINUS
                                                                                                                                                                                                            CRAA_BACUH
                                                                                                                                                                                                                                                                                                                                                                                                                          Saitoh H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                            protein)
                                                                                                                                                                                                                           098597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          crentrhaeon, Aeropyrum pernix Kl.";

DNA Res. 6:83-101(1999).

-!-CATALYTIC ACTIVITY: L-glutamate + H(2)O + NAD(P)(+) = 2-
oxoglutratate + NH(3) + NAD(P)H.

-!- SUBUNIT: HOWOHEXAMER (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE GLU/LEU/PHE/VAL DEHYDROGENASES FAMILY.
264 VRFDGVYISKTTYIRQ----GEQSLDGFYRAWHQVEYYRYI-----RFFPDGHVMMLTTP 314
                          107 HPYEQEVSAL---GGIPYSQIYGWYRVN------FGVIDERL-HRNREYRDRYYRNL 153
                                             : | | : : | || : : | || : | EEPQSIVPRLRTRTDAILLGHYRLSQDTDNQTKVFAVITKKKEEKPLDYKYRYRRRY 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 RPPDEIKRSGGLMPR-----GHNEYF------DRGTQMNINLYDHARGTQTGFVRYDDG 58
                                                                                                                                                                                                                                                                                                                                                                                                          Ή.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 OPTDPLEEARAQLRRAVDLLGYDDYVYEVLANPDRVLQVRVT------IKMDDG 54
                                                                                                                                                                                                                                                                                            Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                           Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Ko Hosoyama A., Fukui S., Magai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oquofi A., Aoki K.-I., Kubota K., Makamura Y., Nomira N., Sako Y., Kikuchi H., "Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                 375 PVQEADQSFHVGLQLCSSGHQRFNKLIWIHHS---CHITYKS-TGET 417
                                                                                 154 NIAPAEDGYR--LAGFPPDHQAWREEPWIHHAPQGCGNSSRTITGDT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMBOEALO7A89DA62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58;
                                                                                                                                                                                                             16-OCT-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glutamate dehydrogenase (EC 1.4.1.3) (GDH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001625; GLFV_dehydrog.
InterPro; IPR001625; MaD_binding.
Pfam; PF00208; GLFV_dehydrog. 1.
PRINTS; PR00082; GLFV_dehydrog. 1.
PRINTS; PR00082; GLFPUDRGRNASE.
PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
Act_craft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.6%; Score 86; DB:
Best Local Similarity 21.9%; Pred. No. 1.8;
Matches 41; Conservative 32; Mismatches
                                                                                                                                                                                  423 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002086; Aldehyde_dehydr.
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99310339; PubMed-10382966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP000061; BAA80383.1; -. HSSP; P96110; 1B26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46697 MW;
                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            423 AA;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                  Aeropyrum pernix
                                                                                                                                                                                                                                                                                                                                                                                          Kawarabayasi
                                                                                                                                                                                AERPE
                                                                                                                                                                                                                                                                                                           Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                  STRAIN-K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP_BIND
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                                                                                                                                                                                             720
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59 YVSTSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGG 118
                                                                                                                                               167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 YDHARGTQTGFVRYDDGYVSTSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVN-DV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 LGVYSPHPYEQEVSALGGIPYSQI---YGWYRVNFGVIDERLHRNREYRDRYYRNLNIAP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "94kDa mosquitocidal toxin from serovar higo.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
                                                                     55 TVKTFLGWRSQHNSALGPYKGGVRYH-----PNV-TMNEVIALSMWTWK---NSLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry27Aa (Insecticidal delta-endotoxin CryXXVIIA(a)) (Crystaline entomocidal protoxin) (94 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    626 YFRARHEHFKYIEFD----TIFSLRNSGQLEEHLL-----HIYY----PNTTKISGDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          671 LLIIDKIEFIPV----GIPLNQTSEGYNTYDQNTNSYNQNYNNYNQNMDTTYQ----P
                                                                                                                                               119 IPYSQIYGWYRVNFGVIDER----LHRNREYRDRYYRNLN-----IAPAEDGYRLAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 AEDGYÄLAGFPPDHQAWREEPWIHHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DFD5313C5B6023E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRYZ7A, OR CRYXXVIIA(A).
Bacillus thuringiensis (subsp. higo).
Bacteria, Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              826 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 84.5; D. Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPITHELIAL CELLS OF INSECTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001178; Endotoxin.
Pfam; PF00555; endotoxin; 1.
Toxin; Sporulation.
SEQUENCE 826 AA; 94434 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB023293; BAA82796.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             -f- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- DISEASE: FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND ANIMALS
INFECTED WITH DECENERATIVE NEUROLOGICAL DISEASES SUCH AS KURU,
CREUTZFELDT-JAKOB DISEASE (CJD), GERSTWANN-STRAUSSLER SYNDROME
(GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
-!- SIMILARITY: BELONGS TO THE PRION FAMILY.
                                                                                                                                                                                                                      5 X 8 AA TANDEM REPEATS OF P-H-G-G-W-G-O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRP27-30 (PROTEASE RESISTANT CORE).
N-LINKED (GLCNAC. . .) (BY SIMILARITY).
NYLINKED (GLCNAC. . .) (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                 Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                       060506;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Major prion protein precursor (PrP) (PrP27-30) (PrP33-35C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPI-anchor; Repeat; Signal.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6299CA000EB8607D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAJOR PRION PROTEIN. REMOVED IN MATURE FORM.
                                                                  254 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPI-ANCHOR.
----KVKRQIFSDYQSEVDIYNRIRD 238
         775 NQDTENMYNQSYNNYNSDNNNYNQNSD 801
                                                                                                                                                                                                              MEDLINE=90158578; PubMed=2406562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 1
67 2
75 3
83 4
91 5
27823 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00291; PRION_1; 1. PROSITE; PS00706; PRION_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M33958; AAA37013.1; -. HSSP; P04925; 1AG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000817; Prion. Pfam; PF00377; prion; 1. PRINTS; PR00341; PRION. SMART; SM00157; PRP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prion; Brain; Glycoprotein;
                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254
231
231
181
197
214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 AA;
                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                       NCBI_TaxID=10029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232
231
90
181
197
179
51
                                                                                                                                                                                                      rissue=Brain
                                                                 PRIO_CRIGR
                                                                                                                                                               Cricetulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROPEP
LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                             RESULT 12
PRIO_CRIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- DISEASE: FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND ANIMALS
INFECTED WITH DEGENERATIVE NEUROLOGICAL DISEASES SUCH AS KURU,
CREUTZFELDT-JAKOB DISEASE (CJD), GERSTWANN-STRAUSSLER SYNDROME
(GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
-!- SIMILARITY: BELONGS TO THE PRION FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 AWREEPWIHHAPQGCGN---SSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSE 229
                                                                                                                             114 SALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYR-NLNIAPAEDGYRLAGFPPDHQ 172
                                                                                                                                                                                   120 AVVGGL-----GGYMLGSAMSRPMLHFGNDWEDRYYRENMNRYPNQVYYR-----PVDQ 168
                                                                                                                                                                                                                                                                                            169 YNNQNNFVH----DCVNITIKQHTVTTTTKGE---NFTETDVKMMERVVEQMCVTQYQKE 221
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cricetulus migratorius (Armenian hamster).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.JUL-1998 (Rel. 36, Created)
15.JUL-1998 (Rel. 36, Last sequence update)
15.JUL-1998 (Rel. 36, Last annotation update)
Major prion protein precursor (PrP) (PrP27-30) (PrP33-35C).
                      DB 1; Length 254;
                                                                         51; Indels
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                   Score 83; DB 1
Pred. No. 1.8;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
h
Similarity 25.0%; Pre
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                                                                       31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10032;
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                   Query Match
Best Local S
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PRIO_CRIMI
                                                                         Matches
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54
63
71
79
87
256 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
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200
182
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01-0CT-1996
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                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-:- DISEASE: FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND ANIMALS
INFECTED WITH DECENERATIVE NEUROLOGICAL DISEASES SUCH AS KURU,
CREUTZFELDT-JAKOB DISEASE (CJD), GERSTWANN-STRAUSSLER SYNDROME
(GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
-:- SIMILARITY: BELONGS TO THE PRION FAMILY.
                                                    BY SIMILARITY.

5 X 8 AA TANDEM REPEATS OF P-H-G-G-G-W-G-
0.
1.
2.
3.
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01.JUN-1994 (Rel. 29, Last sequence update)
01.NOV-1997 (Rel. 35, Last annotation update)
Major prion protein 2 precursor (PrP) (Major scrapie-associated fibril
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Comparative sequence analysis and expression of bovine PrP gene in mouse L-929 cells.";
Virus Genes 6:343-356(1992).
-!- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
-!- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
                                                                                                                                                                                                                                      114 SALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYR-NLNIAPAEDGYRLAGFPPDHQ 172
                                                                                                                                                                                                                                                                    173 AWREEPWIHHAPQGCGN---SSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSE 229
                                                                                                                                                                                                                                                                                   169 YNNQNNFVH----DCVNITIKQHTVTTTKGE---NFTETDVKMMERVVEQMCVTQYQKE 221
                    PRP27-30 (PROTEASE RESISTANT CORE).
N-LINKED (GLCNAC. .) (BY SIMILARITY).
N-LINKED (GLCNAC. .) (BY SIMILARITY).
                                                                                                                                                                                                   22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID-9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yoshimoto J., Iinuma T., Ishiguro N., Horiuchi M., Imamura M.
Shinagawa M.;
                                                                                                                                                                             6.4%; Score 83; DB 1; Length 254; 25.0%; Préd. No. 1.8; tive 20; Mismatches 51; Indels
                                                                                                                                             7B963FC6F77F9D0F CRC64;
 REMOVED IN MATURE FORM.
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          GPI-ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                              Μ¥.;
                                                                                                                                             27855
                                                                                                                                                                             Query Match
Best Local Similarity 25.09
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
254
231
231
181
197
214
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75
83
91
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Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                              254 AA;
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Q01880;
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                     DOMAIN
CARBOHYD
CARBOHYD
                                                       DISULFID
                                                                                                                                             SEQUENCE
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@lsb-sib.ch).
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-!- DISEASE: FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND ANIMALS
INFECTED WITH DEGENERATIVE NEUROLOGICAL DISEASES SUCH AS KURU,
                                                                                                                                                                                                                                                                                                                                                                                                                           MAJOR PRION PROTEIN 2.

N-LIRKED (GLCNAC. ) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

BY SIMILARITY.

5 X 8 AA TANDEM REPEATS OF P-H-G-G-G-W-G-
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Martin T., Hughes S., Hughes K., Dawson M.;
"Direct sequencing of PCR amplified pig PrP genes.";
Blochim. Blophys. Acta 1270:211-214(1995).
-!- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
-!- SHOUNT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED." PROPS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 SALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYR-NLNIAPAEDGYRLAGFPPDHQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 AWREEPWIHHAPQGCGN---SSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSE 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 YSNONNFVH----DCVNITVKEHTVTTTKGE---NFTETDIKMMERVVEQMCITQYORE 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 82; DB 1; Length 256;
Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51; Indels
                                                                                                                                                                                                                                                                SMART; SM00086; PAC; 1.
SMART; SM00157; PRP; 1.
PROSITE; PS00291; PRION_1; 1.
PROSITE; PS00706; PRION_2; 1.
PRION; Brain; Glycoprotein; GPI-anchor; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0D969FF2D9033B30 CRC64;
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(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 170 270 78 3 86 4 95 27880 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.3%;
                                                                         EMBL; D10614; BAA01469.1; -. PIR; JU0268; JU0268. HSSP: P04156; LEIG. InterPro; IPR001610; PAC. InterPro; IPR000817; Prion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30; Conservative
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                                                                                                                                                                                                             Pfam; PF00377; prion; 1 PRINTS; PR00341; PRION.
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184
200
217
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                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
MAJOR PRION PROTEIN.
MAJOR PRION PROTEIN.
MAJOR PROPERTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
5 X 8 AA TANDEM REPEATS OF P-H-G-G-W-G-G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 YSNQNSFVH----DCVNITVKQHTVTTTKGE---NFTETDVKMIERVVEQMCITQYQKE 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 SALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYR-NLNIAPAEDGYRLAGFPPDHQ 172
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CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME (GSS), SCRAPIE, BOVINE SPONGIPORM ENCEPHALOPATHY (BSE), TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), FTC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.3%; Score 82; DB 1; Length 257; Best Local Similarity 24.2%; Pred. No. 2.2; Matches 30; Conservative 21; Mismatches 51; Indels
                                                                                                                                                                                                            HSSP; P04925; 1AG2.
InterPro; IPR000817; Prion.
Pfam; PF00377; Prion; 1.
PRIWTS; PR00341; PR10N.
SWART; SW00157; PRP; 1.
PROSITE; PS00291; PRTON_1; 1.
PROSITE; PS00706; PRION_2; 1.
PROSITE; PS00706; PRION_2; 1.
SPION; Brain; Glycoprotein; GPI-anchor; Repeat; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3A87104B234C55DD CRC64;
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70 2
78 3
86 4
95 27727 MW;
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185
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CARBOHYD
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DOMAIN
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SEQUENCE
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Search completed: June 10, 2002, 17:33:23 Job time: 130 sec

Q9imu3 banna virus Q9vle2 drosophila Q961p3 drosophila Q0398B bacillus sp Q97n09 clostridium

018559 caenorhabdia 090vu7 neurospora 097904 bos javanic 097695 giraffa cam 097655 giraffa cam 096018 emericella 070572 mus musculu 094130 nephroselmi 025050 hyphantria 091912 bison bonas 091144 streptomyce 091144 streptomyce 091144 streptomyce 091275 shigella so 052376 bombyx mori 092395 bombyx mori 092395 bombyx mori 092395 bombyx and

09c209 neurospora 097698 cervus elap P97895 mesocricetu 062670 cervus elap

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"Escherichia coli heat-labile enterotoxin B subunits supplemented with a trace amount of the holotoxin as an adjuvant for nasal influenza vaccine.";

Vaccine.";

Vaccine 12.1083-1089(1994).

EMBL; AB011677; BAA25725.1; -.

HSSP; P06717; LILGG.

InterPro; IPR001144; Enterotoxin_A.

InterPro; IPR001146; Enterotoxin_A.

Pram: PF01375; Enterotoxin_A: 1.

PRINTS: PR00717; ENTERPOTOXINA.

PROSITE: PR00014; ER TARGET; UNKNOWN.1.

SEQUENCE 258 AA; 29931 MW; 2BB15D27740EB788 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=1032 (ENTEROTOXIGENIC);
MEDLINE=95091056; Pubmed=7998417;
Tamura S., Asanuma H., Tomita T., Komase K., Kawahara K., Danbara H.,
Hattori N., Watanabe K., Suzuki Y., Nagamine T., Aizawa C., Oya A.,
Kurata T.;
                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-LABILE ENTEROTOXIN A SUBUNIT.
LTH A SUBUNIT.
Escherichia coli.
Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                      ALIGNMENTS
Q9VLE2
Q9VLE2
Q961P3
Q03988
Q97N09
                                                                           097695
09W0C6
09W0C6
070572
070573
097912
09911E4
09911E4
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09911E4
0992336
0902336
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0902395
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=1032 (ENTEROTOXIGENIC);
                  276
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                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                 353

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066280
047182 escherichia
057372 vibrio chol
09u84 pieris rapa
069258 bordetella
099v36 pieris bras
081497 arabidopsis
02495 galleria me
093v22 bordetella
070057 bordetella
09n557 homo sapien
091557 schizosacch
                                                       June 10, 2002, 17:30:53 ; Search time 26.47 Seconds (without alignments) 1568.522 Million cell updates/sec
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Q95n12 ovis aries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  066280 escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                          US-09-297-171-1
1304
1 NGDRLYRADSRPPDEIKRSG.....QIFSDYQSEVDIYNRIRDEL
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                      hits satisfying chosen parameters:
                                                                                                                                                      562222 seqs, 172994929 residues
                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Q9YB04
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Gapop 10.0 , Gapext 0.5
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SEQUENCE FROM N.A.
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                                     233 YNRIRDEL
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01-NOV-1996
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                                                                                                                                                                                                  STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                         121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
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                          Gaps
                                              1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
                                                          19 NGDKLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto T., Yokota T.;
Sequence of heat-labile enterotoxin of Escherichia coli pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                    Yahamoto T., Tamura T., Ryoji M., Kaji A., Yokota T., Takano T., "Sequence analysis of the heat-labile enterotoxin subunit B gene originating in human enterotoxigenic Escherichia coli."; J. Bacteriol. 152:506-508(1982).
                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
NCBI_TaxID=562;
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   Length 258;
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Score 1290; DB 2;
Pred. No. 1.4e-110;
2; Mismatches 1;
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InterPro: IPR000886; ER_target.
Pfam; PF01375; Enterotoxin_A; 1.
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MEDLINE=83265593; PubMed=6348025;
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J. Bacteriol. 155:728-733(1983).
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047182;
01.002-1996 (TrEMBLrel. 01, Cr
01.007-1996 (TrEMBLrel. 01, La
01-DEC-2001 (TrEMBLrel. 19, La
ENTEROTOXIN A (FRAGMENT).
98.98;
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                         Conservative
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            al Similarity
237; Conserv
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173 AWREEPWIHHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDI 232

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[1]
SEQUENCE FROM N.A.
MEDLINE-99415906; PubMed-10485873;
Watanabbe M., Kono T., Matsushima Hibiya Y., Kanazawa T., Nishisaka N.,
Kishimoto T., Koyama K., Sugimura T., Wakabayashi K.;
Wholecular cloning of an apoptosis-inducing protein, pierisin, from cabbage butterfly: Possible involvement of ADP-ribosylation in its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pterygota, Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia,,
Papilionoidea, Pieridae, Pierinae, Pieris.
                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio...
                                                                                                                                                                                                                                                        Lebens M., Holmgren J.; "Structure and arrangement of the cholera toxin genes in Vibrio cholerae 0139.";
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Parin; PF01375; Enterotoxin_A; 1.

PROSITE: PS00014; ER_TARGET; UNKNOWN_1.

SEQUENCE 46 AA; 5447 MW; 1B6085A02E8889D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                    Last sequence update)
Last annotation update)
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AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    850 AA
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EMBL, X76391, CAA53975.1; --
EMBL, X76390, CAA53974.1; --
HSSP, P01555, 1XTC.
InterPro; IPR001144; Enterotoxin_A.
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EMBL; AB030305; BAA84491.1; -.
Interpro; IPR000772; Ricin_B_lectin.
Pfam; PF00652; Ricin_B_lectin.
SMART; SM00458; RICIN; 4
                                    Created)
                                                                                                                                                                                                                            STRAIN=4260B;
MEDLINE-94237453; PubMed=8181723;
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Best Local Similarity 63.6%;
Matches 28; Conservative
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17,
                                (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. )
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MEDLINE-20428462: pubMed-10971585;
Matsushima Hibiya Y., Watanabe M., Kono T., Kanazawa T., Koyama K.,
Matsushima Hibiya Y., Watanabe M., Kono T., Kanazawa T., Koyama K.,
Sugimura T., Wakabayashi K.;
"Purification and cloning of pierisin-2, an apoptosis-inducing protein
from the cabbage butterfly, Pieris brassicae.";
Eur. J. Biochem. 267:5742-5750(2000).
EMBL; AB037676; BAB13774.1; ...
EINTEFPO: IPRO00772; Ricin_Blectin.
Pfam; PF00652; Ricin_Blectin.
SMART; SM00458; RICIN.3.
                                                                                                                                                                                                                                                                                                                                   65 SLR------SAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYE 110
                                                                                                                                                                                                                                                                                                                111 QEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLN--IAPAEDGYRLAGFP 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 ALGGIPYSQIYGWYRVNFGVIDER-LHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAR-2001 (TrEWBLrel. 16, Created)
01-WAR-2001 (TrEWBLrel. 16, Last sequence update)
01-Cr-2001 (TrEWBLrel. 18, Last annotation update)
PIERISIN-B.
PIERISIN-B.
PIERISONA: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysla;
PADILIONOIGEA; Pieridae; Pierinae; Pieris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 TTKTORNKKKYVWTPRNANRGIVXQYEIY-----APGGVDVNDSFSDASPWPNQMEVA 167
                                                                                                                                                                                                         5 LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 RLYRADSRPPDEIKRSG--GLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVS 61
                                                                                                                                                                                                                                                                      7.1%; Score 93; DB 5; Length 850;
24.1%; Pred. No. 7.1;
tive 30; Mismatches 101; Indels
                                                                                                                           DB 2; Length 269;
                                                                                                                                                          62; Indels
                                                POTENTIAL.
TOXIN SUBUNIT S1.
F6CDC9028E6B08AB CRC64;
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SEQUENCE 850 AA; 97988 MW; 6E6044049D36FE73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           169 PDHQAWREEPWIHHAPQGCGNSSRT----ITGDTCNEETQN 205
                                                                                                                                                                                                                                                                                                                                                                                               7.1%; Score 93; DB 2
24.0%; Pred. No. 1.4;
tive 22; Mismatches
 Pfam; PF02917; Pertussis_S1; 1.
PRINTS; PR01395; BORPETOXINA.
Signal; Toxin.
1 34 POS
                                              34 PO
269 TO
29956 MW;
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Best Local Similarity 24.0%
Matches 53; Conservative
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Best Local Similarity 24.19
Matches 62; Conservative
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                                                SIĞNAL 1
CHAIN 35
SEQUENCE 269 AA;
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Willems R.R.J.;
Willems R.R.J.;
Folymorphism in the Bordetella pertussis virulence factors
P.69/pertactin and pertussis toxin in The Netherlands: temporal trends and evidence for vaccine-driven evolution.";
Infect. Immun. 66:507-675(1998).
EMBL; AJ006155; CAA06897.1;
EMBL; AJ007364; CAA07479.1;
EMBL; AJ007363; CAA07478.1;
EMBL; AJ245366; CAB51472.1;
EMBL; AJ245366; CAB51472.1;
InterPro; IPR003898; Borpert_toxA.
                                                                                                                                            62 TSLSLR-----SAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVS 114
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                                                                                             Gaps
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                              DB 5; Length 850;
                                                           7.2%; Score 94; DB 5; Length 850
23.5%; Pred. No. 5.7;
tive 32; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-HAV, AND AL1561;
Boursaux-Eude C., Thiberge S., Carletti G., Guiso N.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mool F.R.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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the EMBL/GenBank/DDBJ databases
PROSITE; PS50231; RICIN_B_LECTIN; 3.
SEQUENCE 850 AA; 98082 MW; 2C891698B2C0880E CRC64;
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                                                                                          Conservative
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274 IKDKNSFLDLSKNVN 288
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Submitted (MAY-1998) to
                                                Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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(TrEMBLrel. 01, Last sequence update) (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 LSTIYLREYQSKVKRQIFSDYQSEVDIYN 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
PERTUSSIS TOXIN SI SUBUNIT PRECURSOR
     01, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0187; HAEMOCYANIN.
PROSITE; PS00209; HEMOCYANIN_1; 1.
PROSITE; PS00210; HEMOCYANIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000896; Hemocyanin.
Pfam; PF00372; hemocyanin; 1.
                                                                                                  Galleria mellonella (Wax moth).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 PC
702 AF
83703 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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01-NOV-1996 (TrEMBLrel. 01-NOV-1996 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel. ARYLPHORIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1
17
702 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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SIGNAL
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
F9D12.5 PROTEIN.
F9D12.5.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                        216 IWR----VNHPDGGNKDGRSERSTSSYDDLMYGGTGNVQEDTFGDESNNPKPIADGEFMI 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYLPRGWEVNVDLKLFIH-NGKLNKYLAISDGTLKLYNDAKREWGFGQLIPHVTFYNTYG 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 EY--RDRYYRNLNIAPAEDG----YRLA--GFPPDHQAWREEPWIHHAPQGCGNSSRTIT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 EYFDRGTQMNIN--LYDHARGTQTGFVRYDDGYVSTSLSLRSAHLAGQSI--LSGYSTY- 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221 YI----EQDIGSFGAEIFIVKPAQQQEKVTFISN-PPTNVFTWKILHFSILEDKFYYSD
                         174 -WREEPWIHHAPQG--CGNSSRT------ITGDTCNEETQNLSTIYLREY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.0%; Score 91; DB 10; Length 392;
21.5%; Pred. No. 3.7;
ive 44; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The A. thaliana Genome Sequencing Project.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. COLUMBIA;
Waterston R.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
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InterPro; IPR002083; MATH.
Pfan, PF00917; MATH; 3.
SEQUENCE 392 AA; 44367 NW; 56D814E330D4769A CRC64;
                                                                                                                                                                                                                                                                                                 392 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319 WGAAN-----LRLKNORSTNHRQIYT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 GDTCNEETQNLSTIYLREYQSKVKRQIFS 224
                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.5%;
                                                                                                                         QSKVKRQIFSDYQSEVD 231
                                                                                                                                                        272 ESIKDKNSFLDLSKNVN 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45; Conservative
                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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081497;
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Q24995
ID Q24995
AC Q24995
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201 SKDNAYYFYANYSGPLTYEDNENLLSYFIEDIGWNSYYYYFHNRFPFWENGEQLIGPLKE 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 RRGEIYYYVYQKILARYYLERLANGLGEIP------RFNWLD------KYQTSYY 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 RYDDG-YVSTSLSLRSAHLAGQSILS-----GYSTYYIYVIATAPNMFNVNDVLG---- 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 PLLSSYQLPFAQRNDDYYLA-----STORM 333
Eukaryota; Metazoa; Arthropa; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea; Pyralidae; Galleriinae; Galleria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 LYRADSRPPDEIKRSGGLMPRGHN---EYFDRG------TQMNINLYDHARGTQTGFV 53
                                                                                                                                                                                                                                                                                                                                                                   Memmel N.A., Trewitt P.M., Silhacek D.E., Kumaran A.K.;
"Nucleotide sequence and structure of the arylphorin gene from Galleria mellonella.";
Insect Blochem. Mol. Biol. 22:333-342(1992).
EMBL; M73793; AAA74229.1;
HSSP; P04253; ILLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5; Length 702;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARYLPHORIN.
E7590F729DC084EA CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.9%; Score 90.5; DF 20.4%; Pred. No. 9.2; tive 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                569
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SEQUENCE FROM N.A.
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223 V------HVPENRSNSDGSSSSVVKKKRILDMKDSPFIYLTDFDKNVKKINNTE 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFP 168
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                                                                                                                                                                                                                                                                                                                                                                                   2 GDRLYRADSRPPDE----IKRS----GGLMPRGHNEYFDRGTQMNINLYDHARGTQTG 51
                                                                                                                                                                                                                                                                                                                94; Indels 123;
                                                                                                                                                                                                                                                                6.8%; Score 88.5; DB 3; Length 332;
19.0%; Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella pertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CZ, AND 18323;
STRAIN-CZ, AND 18323;
BOUTGBUX-ENGC C., GUJSO N.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ006159; CAA066901.1;
EMBL; AJ006151; CAA06893.1;
HSSP; P04977; 1BCP.
      Storms R.K., Vo D.H., Wang Y.; Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                             Jia Y., Cherry J.M.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, 303205; AAB68310.1; -.
SGD; S0005976; YPLOS5C.
SEQUENCE 332 AA; 37309 MW; C3300ED944003F9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
TOXIN SUBUNIT S1.
4310AFEC460A84F4 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 AA
                                                                                                                                                                                                                                                                                                              38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30016 MW;
                                                                                                                                                                                                                                                                                         19.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1998 (TrEMBLrel. 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, TOXIN SUBUNIT SI PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 -----RQIFSDYQS 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271 SECEKAREVFKESDS 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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35 2
269 AA;
                                                                                                                                                                                                                                                                                            Similarity
                                                                       SEQUENCE FROM N.A.
                                                                                           TRANSPOSON-TY4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella.
NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1998
                                                                                                                                                                                                                                                                                                                60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                         Best Local
Matches 6
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                                                                                                                                                                                                                                                                                                                                   11;
                                                                                  "Polymorphism in the Bordetella pertussis virulence factors
P.69/pertactin and pertussis toxin in The Netherlands: temporal trends
and evidence for vaccine-driven evolution.";
Infect. Immun. 66:670-675(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLR------SAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 QEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLN--IAPAEDGYRLAGFP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---YGAASSYF-----EYVDTYGDNAGRILAGA----LATYO 161
                                                                                                                                                                                                                                                                                                                                                                                                   LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSL 64
                                                Moo1 F.R., VanOirschot H., Heuvelman K., vanderHeide H., Gaastra W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Winnett E., Ahmed A., Bussey H., Fortin N., Friesen J.D., Hall J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                84;
                                                                                                                                                                                                                                                                                       Length 269;
                                                                                                                                                                                                                       SEQUENCE 269 AA; 29974 MW; 3413632345D35FA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 PDHQAWREEPWIHHAPQGCGNSSRT----ITGDTCNEETQN 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 SEYLAHRRIP----PENIRRVTRVYHNGITGETTTTEYSN 197
                                                                                                                                                                                                                                                                                                                                   62;
                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 AA.
                                                                                                                                                                                                                                                                                     6.8%; Score 89; DB
23.5%; Pred. No. 3.4;
tive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
STRAIN-B6;
MEDLINE-98114370; PubMed-9453625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 387:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rPL055C OR LPE17C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSPOSON-TY4;
                                                                Willems R.R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSPOSON-TY4;
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PRELIMINARY;
                                                             Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; WD repeat. SEQUENCE 809 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 CRCVRKFSPD 255
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                   NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-491;
                                                                                                                                                                             STRAIN=972H-;
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qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s:
                                                                                                                                           SLR-----SAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYE 110
                                                                                                                                                                                                                                                             111 QEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLN--IAPAEDGYRLAGFP 168
                                                                                                                                                                                                   90 SRRYTEVYLEHRMQEAVEAERAGRG--TGHFIGYIYEV-RADNNF------ 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 VRYDDGYVSTSLSLRSAHLAGQSILSGY-----STYYIYVIATAPNMFNVNDVLGVYSP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 HPYEQEVSAL---GGIPYSQIYGWYRVN-----FGVIDERL-HRNREYRDRYYRNL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 -----YGAASSYE-----EYVDTYGDNAGRILAGA----LATYQ 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364 VRFDGVYISKTTYIRQ----GEQSLDGFYRAWHQVEYYRYI-----RFFPDGHVMMLTTP 414
                           64
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB-TESTIS:
Ottenwaelder B., Obermaler B., Mewes H.W., Gassenhuber J., Wiemann Submitted (JAN-2000) to the EWBL/GenBank/DDBJ databases.
EMBL; AL137520; CAB70786.1; -.
InterPro; IPR001810; F-Dox.
InterPro; IPR001440; TPR.
                        LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TREMBLrel. 10, Last sequence update)
01-DEC-2001 (TREMBLrel. 19, Last annotation update)
PUTATIVE GUANINE NUCLEOTIDE BINDING PROTEIN BETA SUBUNIT-LIKE.
SPBC609.03.
Schlzosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.7%; Score 88; DB 4; Length 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 NIAPAEDGYR--LAGFPPDHQAWREEPWIHHAPQGCGNSSRTITGDT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      547 AA; 62217 MW; A726EE815A82DF31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVQEADQSFHVGLQLCSSGHQRFNKLIWIHHS---CHITYKS-TGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
HYPOTHETICAL 62.2 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                     SEYLAHRRIP----PENIRRYTHVYHNGITGETTTTEYPN 197
                                                                                                                                                                                                                                                                                                                                                                                169 PDHQAWREEPWIHHAPQGCGNSSRT----ITGDTCNEETQN 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PF00646, F-box, 1. PROSITE, PS50181, FBOX; 1. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKFZP434C0118.
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094527
AC 094527
DT 01-MAY
DT 01-DAY
DF 01-DEC
DB PUTATT
CD SPORTOT
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STRAIN-MC58 / SEROGROUP B;

STRAIN-MC58 / SEROGROUP B;

STRAIN-MC58 / SEROGROUP B;

MEDLINB-201755; PubMed=10710307;

Tettelin H., Saunders N.J. Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBOy R., Peterson J.D., Hickey E.K., Mason W.C., Gwinn M.L., DeBOy R., Peterson J.D., Hickey E.K., Mason T., Clacko A., Parksey D.S., Blair E., Cittone H., Clark B.B., Cotton M.D., Utterback T.R., Khouri H., Oin H., Vamathevan J., Sarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;

"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 GY-----VSTSLSLRSAHLAGQ-----SILSGYSTYYI--YVIATAPNMFNVNDVL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 GVYSPHPYEQEVSALGGI-PYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAED 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 ----NPY---YFAIGGTHPYAFLY------DRRWVK-KSFRDDW--TMNTSPEKD 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 SGDKLIKLFDLDS-----SKEGGM-----DHGMETQTRCWSCALDSVKNIVPCDN 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NGD----RLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDD 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64;
                                                                                                                                                                                                                                                                               Seeger K., Harris D., Wood V., Rajandream M.A., Barrell B.G.; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS):
EMBL; AL035226; CAA22832.1; --
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 5.
SWART; SM00320; WD40; 5.
PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
PROSITE; PS50082; WD_REPEATS_2; 1.
PROSITE; PS50082; WD_REPEATS_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 6.7%; Score 87; DB 3; Length 809; Best Local Similarity 22.6%; Pred. No. 23; Matches 43; Conservative 29; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Complete proteome.
SEQUENCE 145 AA; 16339 MW; 900382FF572BAB3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92498 MW; 4877443546BD057E CRC64;
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN NMB1343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 AA.
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EMBL; AE002482; AAF41718.1;
TIGR; NMB1343; -
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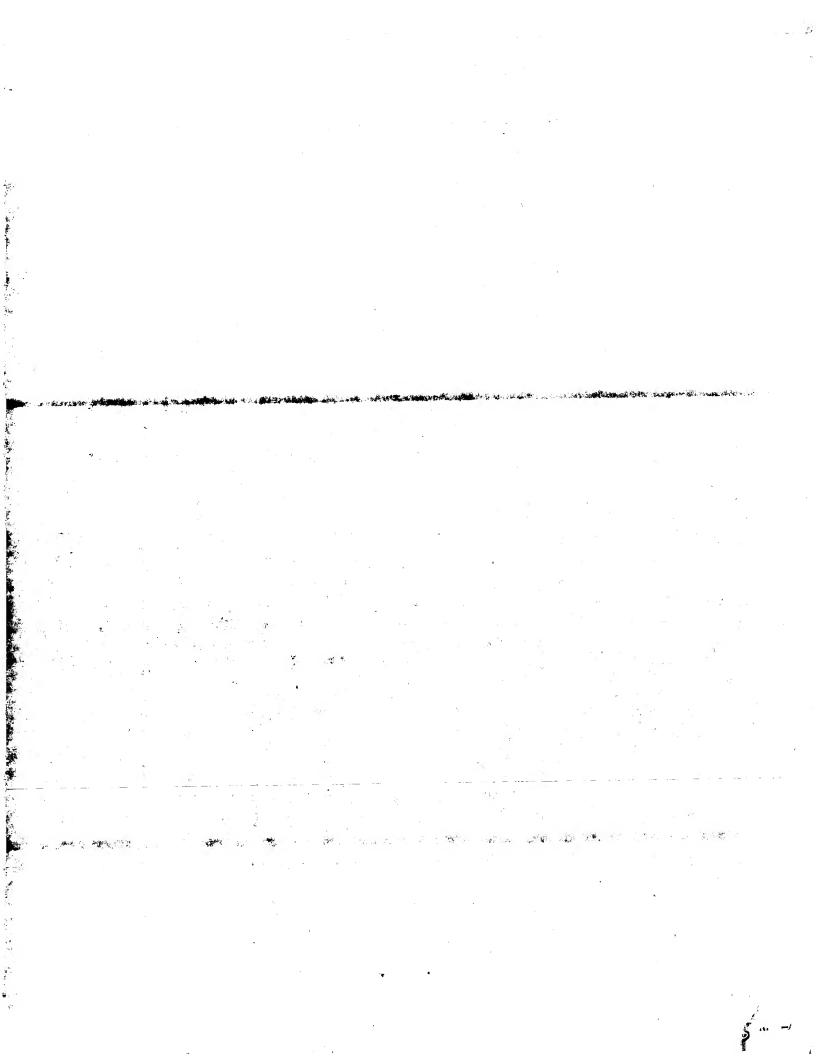
12;

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                                                                                                                                                  113 VSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYR-NLNIAPAEDGYRLAGFPPDH 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 QAWREEPWIHHAPQGCGN---SSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQS 228
                                                                                    Indels 25; Gaps
                                                               2 GDRLYRADSRPPDEIKRSGGLMPRGHN------EYFDRGTQ-MNINLYDHARGTQ 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48; Indels 25; Gaps
                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PRION PROTEIN.
Ovis aries (Sheep).
Ovis aries (Sheep).
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidea; Caprinae; Ovis.
   Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.6%; Score 85.5; DB 6; Length 256; Best Local Similarity 25.6%; Pred. No. 6.6; Matches 32; Conservative 20; Mismatches 48; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1],
SEQUENCE FROM N.A.
Li Y., Tien P.;
Li Y., Tien P.;
"The PrP gene of Chinese little-fat-tail sheep.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY029774; AAR38355.1;
SEQUENCE 256 AA; 27927 MW; 872D78A6CFC6521C CRC64;
Ouery Match 6.6%; Score 86.5; DB 16; Best Local Similarity 29.3%; Pred. No. 2.4; Matches 36; Conservative 15; Mismatches 47;
                                                                                                                                                                                                                                                                                                              256 AA.
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095N12;
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Search completed: June 10, 2002, 17:33:06 Job time: 133 sec

172 YS-NQDNFVH----DCVNITVKQHTVTTTTKGE---NFTETDIKIMERVVEQMCITQYQR 223

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Their Preparation and
                        Sequence 8, Appli
Sequence 16, Appl
Sequence 57, Appl
Sequence 17, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 10, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 10, Appli
Sequence 24, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 26, Appli
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Sequence 3, Application US/08823120

Patent No. 6149919

GENERAL INFORMATION:
APPLICANT: Domenighini, Mario
APPLICANT: Rappuoli, Kino
TITLE OF INVENTION: Immunogenic Detoxified Mutants of
TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Prepa
TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Drepa
TITLE OF INVENTION: Cholera Toxin and of the Propin Lt, Their Drepa
TITLE OF INVENTION: Cholera Toxin and of the Proxin Lt, Their Drepa
TITLE OF INVENTION: Cholera Toxin and of the Proxin Lt, Their Drepa
TITLE OF INVENTION: Cholera Toxin and of the Proxin Lt, Their Prepa
TITLE OF INVENTION: Cholera Toxin and of the Proxin Lt, Their Prepa
TITLE OF INVENTION: Cholera Toxin and of the Proxin Lt, Their Prepa
TITLE OF INVENTION USA
TITLE OF INVENTION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILLING APPLICATION DATA:
APPLICATION USABBE: US/08/823,120
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Pred. No. 1.1e-142;
                     US-08 435-605A-8
US-08 435-605A-16
US-08 435-605A-55
US-08 435-605A-57
US-08 435-605A-17
US-08 435-605A-10
US-08 435-605A-10
US-08 171-299B-11
US-08 171-299B-11
US-09 251-645-6
US-08 260-848A-2
US-08 260-848A-2
US-08 260-467B-10
US-08 462-467B-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,003
FILING DATE: 11-NOV-1994
ATTONNEY/AGENT INFORMATION:
NAME: MCCLUNG, BALDARA G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0315.001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 18FORMATION:
TELEPHONE: (510, 601-2708
TELEPHONE: (51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.6%;
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity
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US-08-823-120-3
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82.5
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                                                                                                                                                                                                         (without alignments)
453.375 Million cell updates/sec
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Sequence 124, App
Sequence 114, App
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                                                                                                                                                                                                                                                                          US-09-297-171-1
1304
1 NGDRLYRADSRPPDEIKRSG......QIFSDYQSEVDIYNRIRDEL 240
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Sequence 2, P
Sequence 2, P
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                                                                                                                                                                              June 10, 2002, 17:15:38 ; Search time 12.93 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-360-107A-124
US-08-404-223B-114
US-08-475-668A-114
US-08-475-668A-114
US-08-471-913A-114
US-08-471-913A-114
US-08-471-913A-114
US-08-471-913A-114
US-08-471-913A-114
US-08-471-913A-114
US-08-471-913A-114
US-08-473-605A-13
US-08-473-605A-2
US-08-473-605A-2
US-08-473-605A-2
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US-08-435-605A-51
US-08-435-605A-55
US-08-435-605A-53
US-08-435-605A-49
US-08-435-605A-49
US-08-435-605A-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hits satisfying chosen parameters:
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-08-435-605A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                231628 segs, 24425594 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
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APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
TITLE OF INVENTION: B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
                  STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                       YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                            181 HHAPQGGGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
                                                                                                                                                                                STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Floppy disk COMPUTER: TBM PC COMPUTER: TBM PC COMPACTION SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/486,090 CLASSIDATE: 07-ITIN-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1183; DB 3;
Pred. No. 3.6e-129;
2; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7872-031
                                                                                                                                                                                                                                                                                      Sequence 114, Application US/08486099 Patent No. 6013263 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: COTUZZÍ, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-1
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELERX: (614) PENNIE
TELEX: 6644 PENNIE
INFORMATION FOR SEQ ID NO: 114:
                                                                                                                                                                                                                                                                                                                                             Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                       Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.7%;
ilarity 93.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    Barney, Shawn O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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Best Local Similarity
Matches 224; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
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APPLICANT:
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                  61
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                                                                                                                             121 YSQIYGWYRVNFGVIDEREHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                                                                                         STSLSLRSAHLAGQSILSGYSIYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                     1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
                                  1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
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   Gaps
                                                                                                                                                                                                                                                    181 HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pizza, Mariagrazia
TITLE OF INVENTION: Immunogenic Detoxified Mutants of
TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their E
TITLE OF INVENTION: Their Use for the Preparation of Vaccines
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
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 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/38/823,120
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Pred. No. 3.2e-129;
 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US .38/256,003
FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 0315.001
TELECOMMUNICATION INFORMATION:
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ISM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                               RESULT 2
US-08-823-120-6
; Sequence 6, Application US/08823120
; Patent No. 6149919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chiron Corporation
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Rappuoli, Rino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: McClung, Barbara G. REGISTRATION NUMBER: 33,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Chicu Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (510 (655-3542)
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 224; Conservative
 Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Emeryville STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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ZIP: 94608-2916
                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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239;
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121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
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ZIP: 10036-2711
                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
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                                                                                                                                                                            RESULT 5
US-08-484-223B-114
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APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
61 STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
                                                  YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI
                                                                                                                      181 HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 254;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FLING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: CCUUZZI, LBUTE A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1183; DB 3;
Pred. No. 3.6e-129;
2; Mismatches 10;
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New York
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                                                                                                                                                                                                                                            Sequence 124, Application US/08360107A Patent No. 6017536 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                               Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
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TELECOMMUNICATION INFORMATION:
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Best Local Similarity 93.3
Matches 224; Conservative
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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ZIP: 10036-2711
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APPLICANT:
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APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Maid, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
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135 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEFWI
                                                                        181 HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL
                                                                                                          195 HHAPQGCGDSSRIITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 254;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASAIFICATION: 435
                                                                                                                                                                                                                                                            Sequence 114, Application US/08484223B Patent No. 6020459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORREY/AGENT IRFORMATION:
NAME: COTUZZI, LAUTA A. REGISTRATION UNUMBER: 30,742
REFERENCE/DOCKET UNMBER: 7872
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
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amino acid
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Matches 224; Conservative
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MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
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121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
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STATE:
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APPLICANT: Matthews, Thomas J.
APPLICANT: Mild, Carl T.
APPLICANT: Mild, Carl T.
APPLICANT: Lambert, Shawn O.
APPLICANT: Lambert, Shawn O.
APPLICANT: Lambert, Stephen R.
APPLICANT: Lambert, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
ANDRESSE:
ANDRE
                                                                                                                               STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
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                                                                                           181 HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #EDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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Pred. No. 3.6e-129;
2; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TORNEY/Abent Andrea A. NAME: Coruzzi, Laura A. REGISTERATION UNDBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                   Sequence 114, Application US/08919597 Patent No. 6054265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 787
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.7%;
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Best Local Similarity 93.3
Matches 224; Conservative
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; MOLECULE TYPE: protein
US-08-919-597-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Bologn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                     RESULT 6
US-08-919-597-114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                      195
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181 HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
                                                                                       HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN -1995
CLASSIFICATION: 424
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93.3%; Pred. No. 3.6e-129;
tive 2; Mismatches 10;
                                                                                                                                                                                                                           Sequence 114, Application US/08475668A

Patent No. 6060065
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHI
TITLE OF INVENTION: TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
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(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 787
REFERENCE/DOCKET NUMBER: 787
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 114:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity 93.34
Matches 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: COMPETITLE OF INVENTION: FUSI
TITLE OF INVENTION: FRAN
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Bd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
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ZIP: 10036-2711
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Sequence 114, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambort, Dennis M.
APPLICANT: Lambort, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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Pred. No. 3.6e-129;
2; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
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NAME: COUUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELERAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
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Best Local Similarity 93.3
Matches 224; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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                        RESULT 9
US-08-471-913A-114
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                                                                                                                                                                                                                                                                                                                                                                                                        CITY:
STATE:
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                                                                                                                                                                            APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Stephen R.
APPLICANT: Lambert, Dennis M.
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
  195 HHAPQGCGDSSRTITGDICNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/485,551A
FILING DATE: 07.JUN 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 90.7%; Score 1183; DB 3; Best Local Similarity 93.3%; Pred. No. 3.6e-129; Matches 224; Conservative 2; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                    SEE: Pennie & Edmonds LLP
1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 78.772
REFERENCE/DOCKET NUMBER: 782-023
TELECOMMUNICATION INFORMATION:
                                                                                                   Sequence 114, Application US/08485551A Patent No. 6068973
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TELERX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERESTICS:
LENGTH: 254 amino acids
TYPE: amino acid
                                                                                                                                                         APPLICANT: Bolognes1, Dani P. APPLICANT: Matthews, Thomas J. APPLICANT: Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
STREET: 115
CITY: New Y
STATE: New
COUNTRY: US
                                                            RESULT 8
US-08-485-551A-114
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Indels

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APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: VIRUS TRANSMISSION
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 254;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1183; DB 4;
Pred. No. 3.6e-129;
2; Mismatches 10;
                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/08435605A; Patent No. 5874287; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
                              Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: COTUZZI, LAUTA A. REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 787
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 90.7
Best Local Similarity 93.3
Matches 224; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
SOFTWARE: Patenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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CITY: New York
STATE: New York
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US-08-435-605A-13
                                                                           APPLICANT:
                                                      APPLICANT:
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                                                                                                                 APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITTLE OF INVENTION: AVORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PA PC COMPATIBLE
COMPUTER: PA PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 90.7%; Score 1183; DB 4;
Best Local Similarity 93.3%; Pred. No. 3.6e-129;
Matches 224; Conservative 2; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/485,264A FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
REFERENCE/DOOKET NUMBER: 7872-021
TELECOMMUNICATION INFORMATION:
Sequence 114, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 114, Application US/08474349A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 114:
                                                                  Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                     New York
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US-08-474-349A-114
                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                    APPLICANT:
APPLICANT:
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Sequence 8, Application US/08823120
Patent No. 6149919
GENERAL INFORMATION:
APPLICANT: Bomenighini, Mario
APPLICANT: Pizza, Mariagrazia
TITLE OF INVENTION: Immunogenic Detoxified Mutants of
TITLE OF INVENTION: Immunogenic Detoxified Mutants of
TITLE OF INVENTION: Their Use for the Preparation of Vaccines
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 YSQIYGWYRVNFGVIDERLHRNREXRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
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81.7%; Pred. No. 3.5e-118;
ive 24; Mismatches 20; Indels
                                                                                                                                                                     COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BIM PC compatible
COMPOTER: BIM PC compatible
COMPOTER: DatentIn Selease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,120
FILING DATE:
CLASSIFICATION NUMBER: US/08/823,120
FILING DATE:
APPLICATION NUMBER: US/08/823,120
FILING DATE:
APPLICATION NUMBER: US/08/256,003
FILING DATE:
ATTORNEY/AGENT INFOWATION:
NAME: MCCLUNG, BATDATA G.
REGISTRATION NUMBER: 33,113
REGISTRATION NUMBER: 33,113
REGISTRATION NUMBER: 33,113
REGISTRATION NUMBER: 33,113
REGISTRATION NUMBER: CATOR
TELEFNIC (510) 601-2708
TELEGTH: SEQUENCE CHARACTERISTICS:
LENGTH: SEAUENCE OF CATOR CATOR CATOR
TOWNE: MATOR CATOR CATOR CATOR CATOR
TOWNE: MATOR CATOR C
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 81.7'
Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: peptide US-08-823-120-4
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CITY: Emeryville
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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APPLICANT: Rappuoli, Rino
APPLICANT: Plaza, Mariagnazia
APPLICANT: Plaza, Mariagnazia
TITLE OF INVENTION: Immunogenic Detoxified Mutants of
TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Preparation and
TITLE OF INVENTION: Their Use for the Preparation of Vaccines
TITLE OF WESTONDENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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83.4%; Score 1088; DB 2; Length 240;
Best Local Similarity 81.7%; Pred. No. 3.5e-118;
Matches 196; Conservative 24; Mismatches 20; Indels
APPLICANT: Burnette, W. Neal
APPLICANT: Kaslow, Harvey
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
STREET.
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA

ZHF: 91320-1789

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,605A
FILING ATTON NUMBER: US/08/435,605A
FILING ATTON NUMBER: US/08/435,605A
FILING ATTON NUMBER: 27,657
REGISTRATION NUMBER: 27,657
REFERENCE/DOCKET NUMBER: A-196B
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:

"PARTY 240 amino acids
                                                                                                                                                                                                                                     STREET: Amgen Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: Us
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STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
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TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: protein
US-08-435-605A-13
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PRIOR APPLICATION DATA:
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APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 83.4%; Score 1088; DB 4; Length 2. Best Local Similarity 81.7%; Pred. No. 3.5e-118; Matches 196; Conservative 24; Mismatches 20; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                              NAME: MCClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERNCE/DOCKET NUMBER: 0315.001
TELECOMUNICATION INFORMATION:
TELEPHONE: (510) 601-27.08
TELEPHONE: (510) 665-3542
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/449,045C
FILING DATE: 24 MAY-1995
CLASSIFICATION: 424
                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,003
FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                          US/08/823,120
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CORRESPONDING ADDRESS:
ADDRESSEE:
STREET: 1840 De Havilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/08449045C; Patent No. 5770203; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-823-120-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Thousand Oaks
STATE: California
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ZIP: 91320-1789
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181 HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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APPLICATION NUMBER: US 07/694,733
FILING DATE: 02-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,222
FILING DATE: 06-JUL-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: June 10, 2002, 17:32:05 Job time: 987 sec
                                                                                                                                                                                         A-196C
                                                                                                                                      NAME: Mazza, Richard J. REGISTRATION NUMBER: 27,657
                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-449-045C-2
                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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Perfect score:

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Sequence:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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sequence 114, App
Sequence 116, Appl
Sequence 116, Appl
Sequence 117, A
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; GENERAL INFORMATION:
APPLICANT: Plaza, Mariagrazia
APPLICANT: Gluliani, Marzia M
APPLICANT: Rappuoll, Rino
TITTLE OF INVENTION: IMMUNGENIC DETOXIFIED MUTANT E. COLI LT-A TOXIN
FILE REFERENCE: 0342.001 / 2302-0342
CURRENT APPLICATION NUMBER: 1999-04-27
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1997-10-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 240
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                                         Seguence
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                                   US-08-471-913-114
US-08-471-913-114
US-08-484-223A-114
US-08-485-546-114
US-08-485-546-114
US-08-485-51-114
US-08-487-266-114
US-08-487-266-114
US-08-487-266-114
US-08-487-355-114
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PCT-US01-08582-3
PCT-US9-3-30747-50
B US-09-470-124-68
B US-09-470-124-48
PCT-US9-30747-48
B US-09-470-124-48
PCT-US9-30747-52
B US-09-470-124-52
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US-09-051-315-2
US-09-423-493-2
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US-09-402-100-4
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US-08-256-003-1
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                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
; ORGANISM: Escherichia coli
US-09-297-171-1
US-09-297-171-1
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Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 2, Appli
                                                                                                                                  ; Search time 108.72 Seconds
(without alignments)
776.999 Million cell updates/sec
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Sequence 3, Appli
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                                                                                                                                                                                                                                                       1 NGDRLYRADSRPPDEIKRSG......QIFSDYQSEVDIYNRIRDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/2/paa/US60_COMB.pep:*
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-255-003-3

US-09-819-917-7

PCT-US99-30747-4

US-09-470-124-4

US-09-256-003-6

US-09-044-696-2
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                                                                                                                                                                                                                                                                                                                                                        3502263 seqs, 351980561 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
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Gaps

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1304 1299 1294 1287 1287 1183

Score

Result Š

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181 HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL
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; OTHER INFORMATION: heat-labile toxin gene mutagenized to optimize
; OTHER INFORMATION: expression in plants.
PCT-US99-30747-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1294; DB 22;
Pred. No. 7.3e-136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
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                                                                                                                                                                                                                                   ; Sequence 7, Application US/09819917; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.28;
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Best Local Similarity 99.28
Matches 238; Conservative
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; ORGANISM: E. coli
US-09-819-917-7
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LENGTH: 259
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APPLICANT: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
TITLE OF INVENTION: Immunospenic Detoxified Mutants of
TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Preparation and
TITLE OF INVENTION: Their Use for the Preparation of Vaccines
CORRESPONDENCE: 41
CORRESPONDENCE ADDRESS:
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181 HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
                                                                                                                                                                                                                                                                                   121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
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99.6%; Pred. No. 2e-136;
***** 1. Mismatches 0; Indels
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COMPUTER READABLE FORM:
*MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
*APPLICATION NUMBER: US/08/256,003
FLING DATE: 11-NOV-1994
CLASSIFICATION: 435
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Best Local Similarity 99.6
Matches 239; Conservative
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TOPOLOGY: linear
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STATE: California
COUNTRY: USA
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US-08-256-003-3
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FILE REPERENCE: 4868/68427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT FILING DARE: 1999-12-22
NUMBER OF SEO ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
APPLICANT: Pizza, Mariagrazia
APPLICANT: Fontana, Maria Rita
APPLICANT: Giannelli, Valentina
APPLICANT: Giannelli, Valentina
APPLICANT: Giannelli, Valentina
APPLICANT: Rappuoli, Rina
TITLE OF INVENTION: Immunogenic Detoxified Mutants Of Cholera Toxin
FILE REFERENCE: CHING112
CURRENT APPLICATION NUMBER: US/09/819,917
CURRENT FILING DATE: 1997-12-28
PRIOR APPLICATION NUMBER: 9513371.6
PRIOR APPLICATION NUMBER: 9513371.6
PRIOR APPLICATION NUMBER: 9513371.6
PRIOR PILING DATE: 1995-66-30
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
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TITLE OF INVENTION: Immunogenic Detoxified Mutants of TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Preparation and TITLE OF INVENTION: Their Use for the Preparation of Vaccines NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 STSLSLRSAHLAGQYILSGYSLTIYIVIA---NMFNVNDVISVYSPHPYEQEVSALGGIP 116
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APPLICANT: DEL GIUDICE, GIUSEPPE
APPLICANT: DEL GIUDICE, GIUSEPPE
APPLICANT: RAPPUGLI, RINO
TITLE OF INVENTION: DETOXIFIED MUTANTS OF BACTERIAL
TITLE OF INVENTION: ADP-RIBOSYLATING TOXINS AS PARENTERAL ADJUVANTS
NUMBER OF SEQUENCES: 4
ADDRESSEE: CHIRON CORPORATION, INTELLECTUAL PROPERTY -
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2; Mismatches 10; Indels
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                                                                                                                                                                                                                          ZIP: 9468-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,003
FILING DATE: 11-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6;
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                                                                                                                            E: Chiron Corporation 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
Pizza, Mariagrazia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: ($10) 601-2708
TELEFAX: ($10 (655-3542)
INPORMATION FOR SEO ID NO: 6:
SEQUENCE CHARACTERISTICS:
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Matches 224; Conservative
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CITY: EMERYVILLE
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                                                                              NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                     CITY: Emeryville
STATE: California
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                                                                                                                              ADDRESSEE:
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APPLICANT: Mason
APPLICANT: Arntzen
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed In
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/84454
CURRENT APPLICATION NUMBER: US/09/470,124
CURRENT FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 259
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                                                                                                                                                                                                                   121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                                                                                                                                                                                       181 HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
                                                                                                                                                                                                                                                                                                                                                                                              200 HHAPQGCGDSSRIITGDTCNEETQNLSIIXLKKYQSKVKRQIFSDYQSEVDIYNRIRNEL 259
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                                                                                                                              20 NGDKLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 79
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                                                                                                     1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
                                                                                                                                                                                                                                                                                                         140 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI
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OTHER INFORMATION: heat-labile toxin gene mutagenized to optimize
OTHER INFORMATION: expression in plants.
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                Length 259;
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                  DB 1;
             Score 1287; DB 1
Pred. No. 5e-135;
4; Mismatches (
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GENERAL INFORMATION:
APPLICANT: Domenighini, Mario
APPLICANT: Rappuoli, Rino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09470124 GENERAL INFORMATION:
                98.7%;
98.3%;
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Matches 236; Conservative
                                    Best Local Similarity 98.3
Matches 236; Conservative
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                Query Match
Best Local
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Gaps

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APPLICANT: Mald, Carl T.
APPLICANT: Mald, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Landbert, Dennis M.
APPLICANT: Landlois, Japhonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
TITLE OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 STSLSLRSAHLAGQYILSGYSLTIYIVIA---NMFNVNDVISVYSPHPYEQEVSALGGIP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
     COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOSAMS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTONREY/AGENT INFORMATION:

NAME: COLUZZI, LAULE A.

REGISTRATION NUMBER: 30,742

REGISTRATION NUMBER: 30,742

REGISTRATION NUMBER: 30,742

REGISTRATION NUMBER: 30,742

REGISTRATION STATEMENTON:

TELEPHONE: (212) 790-9090

TELEPAN: (212) 790-9090

TELEFAX: (212) 790-9090

TELESTA. (212) 869-9741/R864

TELEST. (213) 869-9741/R864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1183; DB 7;
Pred. No. 2.2e-123;
2; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 114 Application US/08470896
GENERAL INFORMATION
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.7%;
Best Local Similarity 93.3%;
Matches 224; Conservative ;
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-360-107-124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
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APPLICANT: Width, Carl T.
APPLICANT: Width, Carl T.
APPLICANT: Barney, Shawn J.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: PRANSMISSION
TITLE OF SEQUENCES: 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Indels
                                                                                 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/39/044,696

FILING DATE: 18-MAR-1993

CLASSIFICATION 1424

PRIOR APPLICATION TABER: US 60/041,227

PILING DATE: 21-MAR-1997

ATONNEY/AGENT INPORMATION:
PLING DATE: 21-MAR-1997

ATONNEY/AGENT INPORMATION:
TELEPHONE: (510) 655-8730

TELEPHONE: (510) 655-8730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.7%; Score 1183; DB 14;
93.3%; Pred. No. 2e-123;
Live 2; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 124, Application US/08360107 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-09-044-696-2
                                                                       COMPUTER READABLE FORM:
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ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                             94662-8097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-360-107-124
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Gaps

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING. SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                    30,742
30,742
7872-030
              UNDER: US/08/471,913
07-JUN-1995
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                                                                                                                   NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-(
TELECAMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPA: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
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APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlais, Alphonse J.
APPLICANT: Langlais, Alphonse J.
APPLICANT: Langlais, Alphonse J.
APPLICANT: Petteway, Stephen R.
APPLICANT: Petteway, Stephen R.
APPLICANT: Petteway, Stephen R.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlais, Alphonse J.
APPLICANT: Langlais, Alphonse J.
ANDINESSE: Pennie & Edmonds
ADDRESSE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLMIAPAEDGYRLAGFPPDHQAWREEPWI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 STSLSLRSAHLAGQYILSGYSLTIYIVIA---NMFNVNDVISVYSPHPYEQEVSALGGIP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12] YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 HHAPQGGGDSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 NGDRLYRADSRPPDEIKRFRSLMPRG-NEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 254;
                                       SOFTABLE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,896
FILING DATE: U6-JUN-1995
CLASSIFICATION: 435
ATTONREY/AGENT INPORMATION:
NAME: CCULZZ, Laura #30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHOME: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
90.7%; Score 1183; DB 8;
Best Local Similarity 93.3%; Pred. No. 2.2e-123;
Matches 224; Conservative 2; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polocial
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 114, Application US/08471913 GENERAL INFORMATION:
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STREET: 1155 Avenue of the A
CITY: New voor
                                                                                                                                                                                                                                                                                                                            TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036-2711
COMPUTER READABLE FORM:
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APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: VINUS TRANSMISSION
TUTLE OF INVENTION: VINUS TRANSMISSION
CORRESPONDENCES: 209
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                 61 STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                195 HHAPQGCGDSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 254
                                                               Gaps
                                                                                                                           1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
                                                                                                                                                           19 NGDRLYRADSRPPDEIKRFRSLMPRG-NEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 77
                                                                                                                                                                                                                                                                                                                                                                   121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI
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                                                               4
      Length 254;
Query Match 90.7%; Score 1183; DB 8; Length 25 Best Local Similarity 93.3%; Pred. No. 2.2e-123; Matches 224; Conservative 2; Mismatches 10; Indels
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us-09-297-171-1.rapm

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NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 781 TELECOMMUNICATION INFORMATION:
                                                                                                                                                  LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                           ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-484-223-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036-2711
COMPUTER READABLE FORM:
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COUNTRY: USA
ZIP: 10036-2711
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APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Barney, Shawn O.
APPLICANT: Langlert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 194
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                                                                                                                                                                                                                                                                                                                                                         Score 1183; DB 8;
Pred. No. 2.2e-123;
2; Mismatches 10;
                                 NAME: Coruzzi, Laura A.
REGISTATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
RELECOMMUNICATION INFORMATION:
FELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEE: Pennie & Edmonds
: 1155 Avenue of the Americas
New York
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 114, Application US/08484223 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           Query Match 90.7%;
Best Local Similarity 93.3%;
Matches 224; Conservative
               ATTORNEY/AGENT INFORMATION NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
                                                                                                                                                                                                                             amino acid
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10036-2711
CLASSIFICATION:
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COUNTRY:
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CITY: N
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TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TITLE OF INVENTION: TRANSMISSION NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 194
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PAPLICATION NUMBER: US/08/484,223A FILING DATE: 07-UW-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 90.7%; Score 1183; DB 8; Best Local Similarity 93.3%; Pred. No. 2.2e-123; Matches 224; Conservative 2; Mismatches 10;
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELERAX: (212) 869-9741/8864
TELERAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 114, Application US/08484223A
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matchews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Albhooste J.
APPLICANT: Langlois, Albhooste J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pennie & Edmonds
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APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
MINMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                          121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
                                                                                                                                                                                                                                                                                                                                                                                 61 STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
                                                                                                                                                                                                                                                                                                                        19 NGDRLYRADSRPPDEIKRFRSLMPRG-NEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 77
                                                                                                                                                                                                                                                          4;
                                                                                                                                                                                                            Length 254;
                                                                                                                                                                                                            Score 1183; DB 8; Length 2
Pred. No. 2.2e-123;
2; Mismatches 10; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/485,546A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 114, Application US/08485546A GENERAL INFORMATION: APPLICANT: Bolognesi, Dani P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (212) 869-9741/8864
3141 PENNIE
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Matthews, Thomas J.
Wild, Carl T.
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NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 78.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                              Query Match 90.7%;
Best Local Similarity 93.3%;
Matches 224; Conservative
                      SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 amino acids
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
    INFORMATION FOR SEQ ID NO:
                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-546-114
                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10036-2711
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                                                               TYPE: amino STRANDEDNESS:
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US-08-485-546A-114
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APPLICANT: Bolognes2, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Matthewst, Dawn O.
APPLICANT: Langlois, Alphone J.
APPLICANT: Langlois, Alphone J.
APPLICANT: Langlois, Alphone J.
APPLICANT: PETERON-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS: ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
STATE: 10036-2711
                                                                                                                                                                                                                                                                                                                      ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                           STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 NGDRLYRADSRPPDEIKRFRSLMPRG-NEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 77
                                                                                                                                                                                                                                                                                                                                                         1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
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                                                                                                                                                                                                                                                                          Length 254;
                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                        Score 1183; DB 8;
Pred. No. 2.2e-123;
2; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-028
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 114, Application US/08485546
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                   TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
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(212) 869-9741/8864
(212) 790-9090
                                                                                                                                                                                                                                                                     90.7%;
illarity 93.3%;
Conservative
                                                                                                   LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                  ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-484-223A-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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Best Local Similarity
Matches 224; Conserv
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TELEPHONE:
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TELEX: 66
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90.7%; Score 1183; DB 8; Length 254;
Best Local Similarity 93.3%; Pred. No. 2.2e-123;
Matches 224; Conservative 2; Mismatches 10; Indels
; TYPE: amino acid
STRANDEDNESS:
; TOPOLOGY: unknown
US-08-485-546A-114
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Search completed: June 10, 2002, 17:35:18 Job time: 210 sec

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Sequence 5679, Ap Sequence 10195, A Sequence 10195, A Sequence 18195, A Sequence 18195, A Sequence 18842, A Sequence 28406, A Sequence 7548, A Sequence 7546, A Sequence 28206, A Sequence 28206, A Sequence 29529, A Sequence 29528, A Sequence 6783, Ap Sequence 62952, A Sequence 62952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1. Application US/09528682
GENERAL INFORMATION:
APPLICANT: Plaza, Mariagrazia
APPLICANT: Plaza, Mariagrazia
APPLICANT: Rappuoli, Rino
TITLE OF INVENTION: IMMORGENIC DETOXIFIED MUTANT E. COLI LT-A-TOXIN
FILE REPERENCE: 2302-0342.10
CURRENT APPLICATION NUMBER: US/09/528,682
CURRENT APPLICATION NUMBER: PJ00-03-20
PRIOR APPLICATION NUMBER: PG7/11997/01440
PRIOR FILING DATE: 1997-10-30
PRIOR PRIOR FILING DATE: 1997-04-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 1
LENGTH: 240
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Pred. No. 3.9e-117;
; Mismatches 0;
US-60-360-039-56743

US-09-540-209B-6743

US-10-096-080-28

US-60-360-039-18195

US-60-360-039-18195

US-60-360-039-2848

US-09-935-625-7848

US-09-935-625-7878

US-09-935-625-7878
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100.0%;
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US-09-528-682-1
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Query Match
Best Local Similarity
   RESULT 2 .
US-09-809-033A-3
US-09-528-682-1
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                                                                                                                             June 10, 2002, 17:32:08 ; Search time 15.77 Seconds (without alignments) 1167.219 Million cell updates/sec
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Sequence 26, Appl
Sequence 7962, Ap
Sequence 630, Appl
Sequence 8, Appl1
Sequence 11030, A
Sequence 4, Appl1
Sequence 4, Appl1
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Sequence 9958, Appli
Sequence 8074, Appli
Sequence 12895, A
Sequence 1788, A
Sequence 4730, Appli
Sequence 7489, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 2, Appli
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1304
1 NGDRLYRADSRPPDEIKRSG.....QIFSDYQSEVDIYNRIRDEL
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1. /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

2. /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3. /cgn2_6/ptodata/2/paa/USO7_NEW_COMB.pep:*

3. /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

3. /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

3. /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

3. /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

3. /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*
                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-540-209B-9958

US-60-360-039-17808

US-60-360-039-4059

US-60-360-039-4730

US-60-360-039-4730

US-60-360-039-7489

US-09-911-345-5

US-10-109-551-10

PCT-US02-13346-3

US-09-602-775C-26

US-09-602-775C-30

US-09-913-345-3

US-09-602-775C-26

US-09-913-345-3

US-09-602-775C-26

US-09-602-775C-30

US-09-913-345-3

US-09-602-775C-30

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                                                                                                                                                                                                                                                                                                                                           233302 segs, 76696041 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listing first 45 summaries
                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
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Match Length
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; Sequence 9958, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: GATY L. Breton
; TITLE OF INVENTION: FOR DIAMOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1001-001
                                                                                        Enterotoxins as Mucosal Adjuvants for Cell-Mediated or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                Yamamoto, Shingo
TITLE OF INVENTION: Chimeric Nontoxic Mutants of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.1%; Score 1084; DB 5;
81.2%; Pred. No. 7.8e-96;
iive 25; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/809,033A
FILING DATE: 16-Mar-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/POCKET NUMBER: McG-01
TELECOMMINICATION INFORMATION:
TELEPHONE: 703/425-8405
INFORMATION FOR SEQ ID NO: 4:
                                                                                                            Humoral Immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRACMENT TYPE: N-terminal
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-809-033A-4
                                                                                                                                                                               and Assoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 382 amino acids
      Takeda, Yoshifumi
                                                                                                                                                                                                STREET: P.O. Box 2509
CITY: Fairfax
                                                                                                                                                                               ADDRESSEE: Hendricks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                      CORRESPONDENCE ADDRESS
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Best Local Similarity
Matches 195; Conserv
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                                                                                  Yamamoto, Shingo
TITLE OF INVENTION: Chimeric Nontoxic Mutants of
Enterotoxins as Mucosal Adjuvants for Cell-Mediated or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 382;
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                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DACA:
APPLICATION NUMBER: US/09/809,033A
FILING DATE: 16-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 83.4%; Score 1088; DB 5; I
Best Local Similarity 81.7%; Pred. No. 3.2e-96;
Matches 196; Conservative 24; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMACION:
NAME: Hendilcks, Glenne
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: McG-01
                                                                                                                                                      Humoral Immunity
                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRACMENT TYPE: N-terminal SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 703/425-8405
TELEFAX: 703/425-8406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09809033A
GENERAL INFORMATION:
APPLICANT: McGhee, Jerry
Kiyono, Hiroshi
                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                            Takeda, Yoshifumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 382 amino acids
McGhee, Jerry
Kivono, Hiroshi
                                                                                                                                                                                                                                      STREET: P.O. Box 2509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                    ZIP: 22031
COMPUTER READABLE FORM:
                                                                  Ohmura, Mari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                              CITY: Fairfax
                                                                                                                                                                                                                                                                                                      ns
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                                                                                                                                                                                                                                                                                                      COUNTRY:
  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-09-809-033A-4
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Sequence 17808, Application US/60360039
Sequence 17808, Application US/60360039
GENERAL INFORMATION:
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Gladman, Barry S.
APPLICANT: Blatch Seven C.
APPLICANT: Blatch Seven C.
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38 -10(52052)A
FILE REFERENCE: 38 -10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 17808
                                                                                                                                                                                                          APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: HINTE, Gregory J.
APPLICANT: Stater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT APPLICATION NUMBER: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 YVSTSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 IPYSQIYGWYRVNFGVIDER----LHRNREYRDRYYRNLN-----IAPAEDGYRLAGF 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 RPPDEIKRSGGLMPR----GHNEYF-----DRGTQMNINLYDHARGTQTGFVRYDDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 OPTDPLEEARAQLRRAVDLLGYDDYVYEVLANPDRVLQVRVT-----IKMDDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 423;
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; OTHER INFORMATION: unsure at all Xaa locations
US-60-360-039-17808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.6%; Score 86; DB Best Local Similarity 21.9%; Pred. No. 2.4; Matches 41; Conservative 32; Mismatches
                                                                                                                                                      ; Sequence 22895, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
    188 GN-SSRTITGDTCNEETQNLSTIYL 211
                                             671 DNLKVRASWGKLGNSEIGNYEYMWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRGANISM: Aeropyrum pernix
US-60-360-039-22895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 PPDHQAW 174
                                                                                                               RESULT 6
US-60-360-039-22895
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US-60-360-039-17808
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Sequence 8074, Application US/09540209B

GENERAL INFORMATION:
APPLICANT: GATY L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRATILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
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                                                                                                                                                                                                                                                                                                                                                                                                                                    510 PAYOTRFSDGVIVDGITPPSQ----LSTSFGYESNYSY---TLENLLNYH------HT 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 ----NREYRDRYYRNLNIAPAEDG-----YRLAGFPPDHQAWR--EEPWIHHAPQGC 187
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                                                                                                                                                                                                                                                              90; Gaps
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                                                                                                                                                                                                                     Length 1119;
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21.5%; Pred. No. 4.8;
ive 28; Mismatches
                                                                                                                                                                                                                   Query Match 6.8%; Score 89; DB Best Local Similarity 22.2%; Pred. No. 4.4; Matches 60; Conservative 25; Mismatches
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                                                                                                                                                                                                                                                                                                       12 PPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHAR--
CURRENT APPLICATION NUMBER: US/09/540,209B CURRENT FILING DATE: 2000-04-04 NUMBER OF SEQ ID NOS: 10444 SEQ ID NO 9958
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Best Local Similarity 21.5%
                                                                                                          ; TYPE: PRT
; ORGANISM: B.fragilis
US-09-540-2098-9958
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US-09-540-209B-8074
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A.
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 4059
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GENERAL INFORMATION:
APPLICANT: Cao, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Glodman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE PERERECE: 38-10(52052)A
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                                                                                                                                                                                                                                                                               59 YVSTSLSLRSAHL--AGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSAL 116
                                                                                                                                                                                                                                                                                                                                                                                                                         ---PYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAE 159
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                                                                                                                                      6 YRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHAR-----GTQTGFVRYDDG 58
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                                                                        46; Indels 100;
                                                                                                                                                                                     DB 7; Length 1095;
Length 875;
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DB 7;
9.5;
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                                                                    17; Mismatches
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Score 84;
Pred. No. 9
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GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
6.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRGANISM: Neurospora crassa
US-60-360-039-4059
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Best Local Similarity 25.28
Matches 34; Conservative
                                                                    47; Conservative
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                                    Similarity
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Query Match
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APPLICANT: Cao, Yongwel
APPLICANT: Cao, Yongwel
APPLICANT: Cao, Yongwel
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 H--KODTSAAHGEPLGVEEVALAKKAYGWPEDKFFYVPDGVHERFAAGIGARGKAAREEW 322
                                                                                                                                                                                                                                                                                                                                                                                                85 DGNPTDGPAVSLDDIEHFROMGSKIPGHPEYRMTTGVETTTGPLGOGLGNSVGMAMAARW 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 RDRY-----YRNL--NIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQGCGNSSRTITGD 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 121;
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                                                                                                                                                                                                                                                                                                    33; Mismatches
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                                                                                                                                                                                                                                                   Score 81.5;
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 4730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7489, Application US/60360039 GENERAL INFORMATION:
                                                                                                                                                  Burkholderia fungorum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Burkholderia cepacia
US-60-360-039-7489
                                                                                                                                                                                                                                           6.2%;
                                                                                                                                                                                                                                           Query Match 6.2%
Best Local Similarity 19.1%
Matches 58; Conservative
                                                                                                                                               ; ORGANISM: Burkl
US-60-360-039-4730
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                          204 TDLAYSDDVETRFRGYNWHTLHVSDANDAAALEAAFVEAKSITDRPILLVVHSIIGWGAP 263
                                                                                                                123 AVVGGL-----GGYMLGSAMSRPLIHFGSDYEDRYYRENMHRYPNQVYYR-----PVDQ 171
                                                                                                                                                                      146 RDRY----YRNL--NIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQGCGNSSRTITGD 197
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                                                                                   107 HPYEQEVSALGGIPY-----SQIYGWYRVNFGVIDERLHR-------NREY
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GENERAL INFORMATION:
APPLICANT: DUNNE, PATRICK W.
APPLICANT: PIEDRAHITA, JORGE
TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TO TRANSMISSIBLE
TITLE OF INVENTION: SPONGIFORM ENCEPHALOPATHIES
FILE REFERENCE: TAMK:20708
CURRENT APPLICATION VIMBER: US/10/109,551
CURRENT FILING DATE: 2002-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.2%; Score 81; DB 5; Length 256; Best Local Similarity 24.2%; Pred. No. 3.7; Matches 30; Conservative 21; Mismatches 51; Indels
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APPLICANT: Langeveld, Joannes P.M.
APPLICANT: Sants, Marinus A.
APPLICANT: Sants, Marinus A.
APPLICANT: Sants, Marinus A.
APPLICANT: Schreuder, Bram E.C.
APPLICANT: Bossers, Alexander
TITLE OF INVENTION: Prion Test
FILE REFERENCE: 2183-50340S
CURRENT APPLICATION NUMBER: US/09/913,345
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: PP 99200391.3
PRIOR APPLICATION NUMBER: PP 99200391.3
PRIOR FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
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GENERAL INFORMATION:
APPLICANT: Garssen, Gerrit J.
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; ORGANISM: Bos taurus
US-09-913-345-5
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173 AWREEPWIHHAPQGCGN---SSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSE 229
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Sequence 10, Application US/10109551

GENERAL INFORMATION:
APPLICANT: PIEDRAHITA, JORGE
TITLE OF INVENTION: TRANSGENCE ANIMALS RESISTANT TO TRANSRIBLE
TITLE OF INVENTION: SPONGIFORM ENCEPHALOPATHIES
TITLE OF INVENTION: SPONGIFORM ENCEPHALOPATHIES
CURRENT APPLICATION NUMBER: US/10/109,551
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/280,549
PRIOR PILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
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24.2%; Pred. No. 3.7;
tive 21; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                  6.2%; Score 81; DB 6; Length 256
24.2%; Pred. No. 3.7;
tive 21; Mismatches 51; Indels
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.; GENERAL INFORMATION:
PPELICANT: Prusiner, Stanley B.
; APPLICANT: Peretz, David
PRIOR APPLICATION NUMBER: 60/2
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 256
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 24.2%
Matches 30; Conservative
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Best Local Similarity 24.28
Matches 30; Conservative
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ORGANISM: Cervus elaphus
US-10-109-551-10
                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Bos taurus
US-10-109-551-2
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LENGTH: 256
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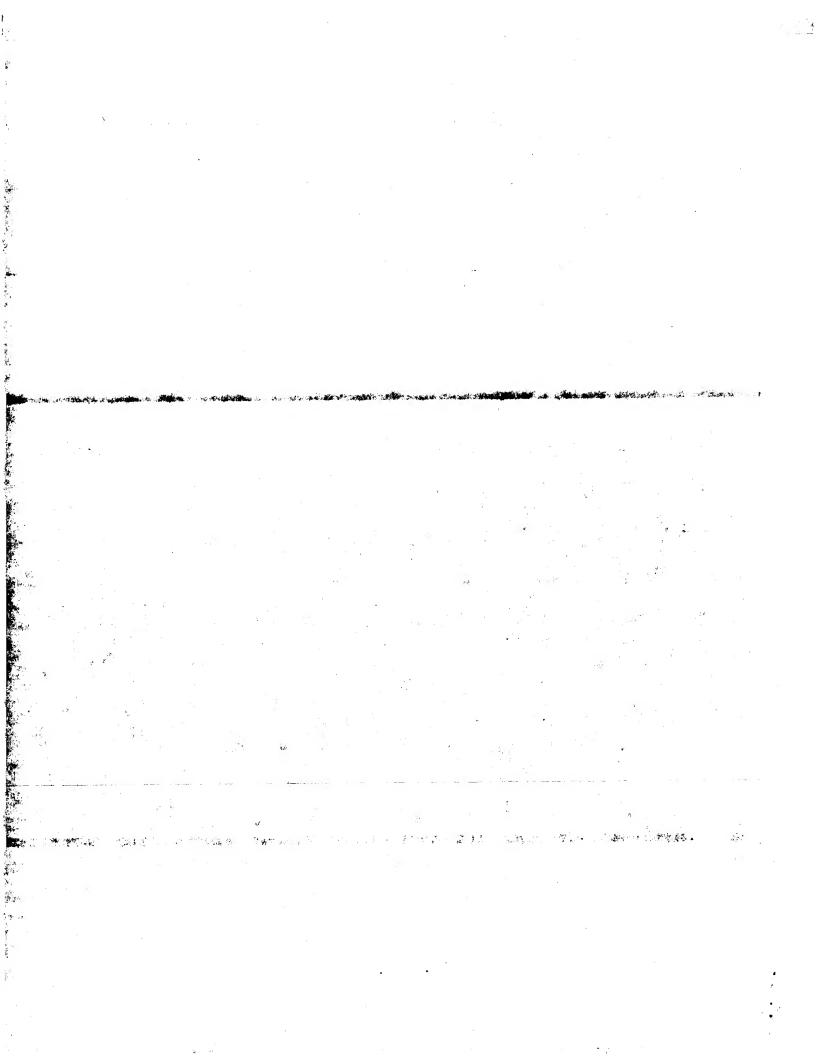
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APPLICANT: Williamson, R. Anthony
APPLICANT: Button, Dennis R.
TITLE OF INVENTION: ANTIBODIES ABOLISH PRION PROPAGATION AND
TITLE OF INVENTION: PROMOTE CLEARANCE OF INFECTIVITY
TITLE OF INVENTION: PROMOTE CLEARANCE OF INFECTIVITY
FILE REFERENCE: UCAL-244WO
CURRENT APPLICATION NUMBER: EQC/202/13346
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 60/287,971
PRIOR FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
LEMCTH: 263
TYPE: PRT
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## APPLICANT: Paramithiotis,
## APPLICANT: Baramithiotis,
## APPLICANT: Baramithiotis,
## APPLICANT: Blon-Usakiewicz, Jacek
## APPLICANT: Haddighat, Ashkan
## APPLICANT: Hand, Marc
## APPLICANT: Lawton, Trebor
## TTILE OF INVENTION: PRION PROPEIN PEPTIDES AND USES THEREOF
## TTILE OF INVENTION: PLION DO COURSENT APPLICATION NUMBER: US/09/602,775C
## CURRENT APPLICATION NUMBER: US/09/602,775C
## CURRENT PILING DATE: 1999-06-23
## PRIOR FILING DATE: 1999-06-23
## SOPTWARE: FastSED for Windows Version 4.0
## SORTWARE: AS TO COURSE SEQUENTION OF THE SEQUENTIAL SEQUENTION OF THE SEQUENTIAL SEQUENTIA
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Best Local Similarity 24.28
Matches 30; Conservative
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PCT-US02-13346-3
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RESULT
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22: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
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240
1 NGDRLYRADSRPPDEIKRSG......QIFSDYQSEVDIYNRIRDEL 240
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Listing first 45 summaries
                                                                                                                                                  OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence encoded b	Plant-optimized E.	Plant-optimized E.	Sequence encoded b	E. coli heat-labil	E. coli heat-labil	Synthetic E. coli	Plant-optimized E.	Plant-optimized E.	Plant-optimized E.	E. coli LT-A prote
SUMMARIES		ΙĐ								AAY96650	AAY96649	AAY96651	AAW65074
		DB	9	71	21	9	22	22	21	21	21	71	19
		Match Length DB I	258	259	259	258	382	380	259	259	259	259	240
ď	Query	Match	100.0	76.7	76.7	74.6	73.8	53.3	52.1	52.1	48.3	48.3	46.2
		Score	240	184	184	179	177	128	125	125	116	116	111
	Result	No.	П	7	ო	4	ស	9	7	8	σ	10	1

Disclosure; Fig 1; 61pp; English.

19 AAW65075 /- 14 AAR44016 /-	0		8	0																									
AAW6507 AAR4401	0	18	œ ·	_																									
	AAR44	AAR4401	^	m 1	AAR38731	2 5	AAU14105	AAR44020	AAR44021	AAR44022	AAR44023	AAR44019	AAR44024	AAR44025	AAR44030	AAR44027	AAR44028		AAR44031	AAR44032	m	AAR38729	AAW80809	AAW80807	AAW67773	AAY96653	S	AAY96655	AAY96656
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12 13	14	15	16	17	18	50	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43

## ALIGNMENTS

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Sequence encoded by the pig scours heat labile toxin (LT) LTA gene.
                                                                                                                                                                                                                                                             New toxoid as inactivated form of toxin for use in vaccines - is obtd. from Organism transformed by gene
                                                                               Pig scours vaccine; toxin; diarrhoea
        AAP50190 standard; Protein; 258 AA.
                                                                                                                                                                                                                 Ross GW;
                                                                                                                                                        84EP-0308620.
                                                                                                                                                                           83GB-0033131.
                                           30-OCT-1991 (first entry)
                                                                                                                                                                                             (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                Hayes MV, Harford S,
                                                                                                                                                                                                                                 WPI; 1985-148358/25.
N-PSDB; AAN50205.
                                                                                                E.coli NCIB 11932
                                                                                                                                                        12-DEC-1984;
                                                                                                                                                                           12-DEC-1983;
                                                                                                                                     19-JUN-1985.
                                                                                                                   EP145486-A.
                         AAP50190;
AAP50190
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Heat-labile
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                                                                                                                                                                                                                                                                                                                                                                                                                  ó
AANSO205 is the gene sequence of the natural LTA gene. The LTA gene of the site directed mutant SDM1 (see AANSO206) is inactive. The inventors claim a vaccine prepn. active against pig scours which contains an inactivated LTA component, together with additional K88 antigens opt. with whole cells comprising the antigens or contg. the inactivated LTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral;
adjuvant; anti-bacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 HHAPQGCGNSSRTITGDTCNEHTQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL
                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                 Length 258;
                                                                                                                                                                                                                                                                                                                                          Score 240; DB 6; Length 2
Pred. No. 1.2e-238;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant-optimized E. coli heat labile toxin A subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.259
/label- mature_protein
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(ARNI/) ARNIZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                          100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                           240; Conservative
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N-PSDB; AAA51106.
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 240; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heat-labile toxin;
                                                                                                                                                                                                                                      258 AA;
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This synthetic Escherichia coli heat-labile toxin (LT) A subunit (LT-A) is encoded by a plant-codon optimized cDNA. The cDNA sequence contains plant-preferred codons and elliminates sequence motifs associated with spurious mRNA processing. A single codon insertion (GTG encoding value) was made to accomodate the creation of a NCoI restriction site around the initiator methionine codon. Novel polymucleciides encode a mutant LT-A polypeptide or a mutant vibrio cholerae cholera toxin (CT) As subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible prophylactic or therapeutic treatment against E. coli or V. cholerae. The mutant polypeptides are also useful as adjuvants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.7%; Score 184; DB 21; I
100.0%; Pred. No. 5.4e-181;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= R192G
/note= "Wild-type arginine is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant-optimized E. coli LT-A G192 mutant.
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/label= signal_peptide
20..259
/label= mature_protein
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Example 1; Fig 1; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 76.7
Best Local Similarity 100.
Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
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of the site directed mutant SDM1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                       the wild type arginine was replaced with glycine at residue 10. The wild type arginine was replaced with glycine at residue 10. Of the mature protein, which was caused by a codon change of TCC to AAG in the coding sequence. The sequence contains plant-preferred codons and alminates sequence motifs associated with spurious mRNA processing. A single codon insertion (GTG encoding value) was made to accompante the creation of a Ncol restriction site around the initiator methionine codon. Novel polynucleotides encode a mutant UT-A polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide. Which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce acidle vaccines, especially oral vaccines in transgenic plants for the prophylactic or therapeutic treatment against E. Coli or V. cholerae. The mutant polypeptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NB: This sequence does not appear in the specification, it was made from the wild type sequence shown in AAY96647, which appears in Figure 1.
                                                                                                                                                                                                                                              This is mutant R192G Escherichia coli heat-labile toxin (LT) A subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPYSQI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                   New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence encoded by the pig scours heat labile toxin (LT) LTA gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.7%; Score 184; DB 21; Length 259; 100.0%; Pred. No. 5.4e-181; tve 0; Mismatches 0; Indels (
                                                  (BOYC-) BQYCE THOMPSON INST PLANT RES
                                                                                                                                                                                                                     Example 3; Page -; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP50191 standard; Protein; 258
                        98US-0113507.
99WO-US30747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         also useful as adjuvants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 76.7
Best Local Similarity 100.
Matches 184; Conservative
                                                                                                    Mason HS, Arntzen CJ;
                                                             (MASO/) MÄSON H S.
(ARNT/) ARNTZEN C J.
                                                                                                                            WPI; 2000-442653/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 AA;
                                                                                                                                          N-PSDB; AAA51544
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                        22-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAP50191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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62 TSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AANSO205 is the gene sequence of the natural LTA gene. The LTA gene can directed mutant SDM1 (see AANSO206) is inactive. The inventors claim a vaccine prepr. active against pig scours which contains an inactivated LTA component, together with additional K88 annigens opt. with whole cells comprising the antigens or contg. the inactivated LTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heat-labile enterotoxin; LT; LTS63Y; LTdell10/112; mutant; detoxified and immunologically active protein; ADP-ribosylation; GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New toxoid as inactivated form of toxin for use in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E. coli heat-labile enterotoxin (LT) mutant LTS63Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.6%; Score 179; DB 6; L4
100.0%; Pred. No. 7.6e-176;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      obtd. from organism transformed by gene
                                                                                                                            /note= "Ser in native
Pig scours vaccine; toxin; diarrhoea
                                                                            Location/Qualifiers 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU00506 standard; Protein; 382 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           larity 100.0%; P
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                        Ross GW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Fig 2; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli strain K88ac.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endotoxin; diarrhoea; mutein.
                                                                                                                                                                                                                                                                                                83GB-0033131.
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                                                                                                                                                                                                                                                                                                                                           (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                      Hayes MV, Harford S,
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1985-148358/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 179; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 AA;
                                      E.col1 NCIB 11932
                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAN50206
                                                                                                   Misc-difference
                                                                                                                                                                                                                                                        12-DEC-1984;
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                                                                                                                                                                                                             19-JUN-1985
                                                                                                                                                                      EP145486-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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us-09-297-171-1.oligo.rag

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enterotoxin (LT) mutant LTS63Y. LTS63Y and LTdell10/112 (AA000507)
are two novel detoxified and immunologically active proteins (LT
mutants) derived by site-directed mutagenesis of the Al subunit of wild
type LT. The substitution of Sar to Tyr at position 63 in LTS63Y blocks
NAD-binding, Delletion of Glu residues at positions 110 and 112 in
LTdell10/112 eliminate the enzymatic activity of LT. The Al subunit of
wild type LT catalyses ADP-ribosylation of Gs, a GTP-binding protein that
regulates CAMP levels. The resulting increase in CAMP is the cause of
diarrhoea in humans and animals e.g. pigs The mucosal immunogenicities
of mutant heat-labile endotoxins LTS63Y and LTdell10/112 were tested.
Groups of mice were immunised with LTS623Y or LTdell10/112. The control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New detoxified mutants of Escherichia coli heat-labile enterotoxin
useful as vaccine for preventing and treating diarrhoea, and as adjuvant
for antibody production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    groups received phosphate buffered saline (PBS) alone. The serum and faecal antibody titres to LT were determined. The results showed that mice immunised with LTSG3Y or LTGell10/1/12 contained high and comparable level of anti-LT antibodies in sera and faecal extracts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              compared with those immunised with wild-type LT. The LT mutants are useful as a vaccine for preventing and treating diarrhoea and as an
                                                                                                                                                                                                                                     'note" "Important residue for enzymatic activity"
                                                                                                                                                                                                                                                                           'note" "Important residue for enzymatic activity"
                                                                                                                                                                'note- "Important residue for enzymatic activity"
                                                     'note= "Important residue for enzymatic activity"
                                                                                       "Important residue for enzymatic activity"
                                                                                                                                                                                                    'note= "Substitution of wild type Ser to Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents Escherichia coli heat-labile
                                                                                                                          note= "Forms the NAD-binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chung S;
                                                                                                                                                                                                                                                                                                             /note= "Encoded by TG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yum J,
                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 39-41; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adjuvant for antibody production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chang J,
                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-KR00555
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                                                                                         note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Park EJ, 'Kim JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-281524/
N-PSDB; AAS01505.
                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                                          Misc_feature
                                  Misc_feature
                                                                      Misc_feature
                                                                                                                                               Misc_feature
                                                                                                                                                                                                                     Misc_feature
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                                                                                                          Region
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Length 382; Indels Score 177; DB 22; I Pred. No. 1.2e-173; 0; Mismatches 73.8%; Scc. 100.0%; Pre 0; 1 Conservative al Similarity 177; Conserv Sequence Query Match Local Best Loca Matches

LSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPYSQ 123 

> g δ

IYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEDWIHHA 183 124

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142 iygwÿrvnfgviderlhrnreyrdryyrnlniapaedgyrlagfppdhgawreepwihha 201
                                                                                                                                                Heat-labile enterotoxin; LT; LTS63Y; LTdell10/112; mutant;
detoxified and immunologically active protein; ADP-ribosylation; Gs;
                  184 PQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
                                                                                                                                                                                                                                           'note= "Important residue for enzymatic activity"
                                                                                                                                                                                                                                                                              'note= "Important residue for enzymatic activity"
                                                                                                                                                                                                                           'note= "Important residue for enzymatic activity"
                            E. coli heat-labile enterotoxin (LT) mutant LTdell10/112.
                                                                                                                                                                                                                                                            "Forms the NAD-binding site"
                                                                                                                                                                                                                                                                                              /note= "Encoded by TG"
                                                                                                                                                                                                          Location/Qualifiers
                                                                             AAU00507 standard; Protein; 380 AA.
                                                                                                                                                                                 Escherichia coli strain K88ac
                                                                                                                                                                   endotoxin; diarrhoea; mutein.
                                                                                                                                                                                                                                                                                                                                                                  99WO-KR00555
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                                                                                                                                                                                                                                                      58..72
/note=
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                                                                                                                                                                                                                   Misc_feature
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                                                                                                                                                                                          Synthetic
                                                                                              AAU00507;
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                                                                    AAU00507
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New detoxified mutants of Escherichia coli heat-labile enterotoxin useful as vaccine for preventing and treating diarrhoea, and as adjuvant for antibody production

ŝ Chung

Yum J,

Park EJ, Kim JS, Chang J,

WPI; 2001-281524/29. N-PSDB; AAS01506.

(MOGA-) MOGAM BIOTECHNOLOGY RES INST.

Claim 6; Page 42-44; 48pp; English.

The present sequence represents Escherichia coli heat-labile enterotoxin (LT) mutant LTdell10/112. LTS63Y (ANU00506) and LTdell110/112 are two novel detoxified and immunologically active proteins (LT mutants) derived by site-directed mutagenesis of the Al subunit of wild type LT. The substitution of Ser to Tyr at position 63 in LTS63Y blocks NAD-binding. Deletion of Glu residues at positions 110 and 112 in LTdell110/112 eliminate the ensymatic activity of LT. The Al subunit of wild type LT catalyses ADP-ribosylation of Gs, a GTP-binding protein that regulates cAMP levels. The resulting increase in CAMP is the cause of diarrhoea in humans and animals e.g. pigs. The mucosal immunogenicities of mutant heat-labile endotoxins LTS63Y and LTdell10/112 were tested. Groups of mice were immuniscal with LTS629 or LTdel110/112. The control groups received phosphate buffered saline (PBS) alone. The serum and faecal antibody titres to LT were determined. The results showed that mice immunisced with LTS639 or LTdel110/112 contained high and comparable level of anti-LT antibodies in sera and faecal extracts

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Gaps

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Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY96650;
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                             Heat-labile toxin; LT-B; mutein; transgenic plant; vaccine; oral;
adjuvant; anti-bacterial; S63K.
                                                                                                                                           113 VSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHO 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals
                                                                                       Gaps
compared with those immunised with wild-type LT. The LT mutants are useful as a vaccine for preventing and treating diarrhoea and as an adjuvant for antibody production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label- 563K
/note= "Wild-type serine is replaced by lysine"
                                                                                      ö
                                                                  Length 380;
                                                                                    Indels
                                                                 Score 128; DB 22; I
Pred. No. 3.4e-123;
                                                                                       .;
0
                                                                Query Match 53.3%; Score 128; DB Best Local Similarity 100.0%; Pred. No. 3.4 Matches 128; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           [..19
/label= signal_peptide
/note= "20"
                                                                                                                                                                                                                                                                                                                                                                                                                         20..259
/label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BOYC-) BOYCE THOMPSON INST PLANT RES.
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                  AAY96647 standard; Protein; 259 AA.
                                                                                                                                                                                                                                                                                                          Synthetic E. coli LT-A K63 mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page -; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US30747
                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mason HS, Arntzen CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MASO/) MASON H S. (ARNT/) ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-442653/38.
                                       380 AA;
                                                                                                                                                                                 233 YNRIRDEL 240
                                                                                                                                                                                             11111111
249 ynrirdel 256
                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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                                       Seguence
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AAY96647
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This is mutant S63K Escherichia coli heat-labile toxin (LT) A subunit (LT-A). The wild-type serine was replaced with lysine at residue 63 of the mature protein, which was caused by a codon change of TCC to AAG in the coding sequence. The sequence contains plant-preferred codons and eliminates sequence motifs associated with spurious mRNA processing. A single codon insertion (GTG encoding value) was made to accomodate the creation of a NcoI restriction site around the initiator methionine codon. Novel polynucleotides encode a mutant LT-A polypeptide or a mutant Vibrio cholerae cholera toxin (GT) A subunit (GT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic coll sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible vaccines, especially creatment against E. coli or V. choleres The mutant polypeptides are used to be a subunit coll to the prophylactic or therapeutic creatment against E. coll or V. choleres The mutant polypeptides are used to be appeared to be a subunit coll or v. choleres the mutant polypeptides are used to be a subunit coll or v. choleres the mutant polypeptides are used to be appeared to the prophylactic or therapeutic creatment against E. coll or V. choleres The mutant polypeptides are used. The mutant polypeptides are used to the propertion of plants to the propertion of plants of the propertion of plants of the propertion of the propertion of plants of the properties of the p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NB: This sequence does not appear in the specification, it was made from the wild type sequence shown in AAY96647, which appears in Figure 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= R192G
/note= "the wild type arginine is replaced by glycine
at position 192 of the mature sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 LSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPYSQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= S63K
/note= "the wild type serine is replaced by lysine
/note= at position 63 of the mature sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.1%; Score 125; DB 21; 100.0%; Pred. No. 2.9e-120; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant-optimized E. coli LT-A A63K+R192G mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= signal_peptide
20..259
/label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 52.1
Best Local Similarity 100.
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 211
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adjuvant; "anti-bacterial; A72R.
                            Sscherichia coli.
                                          Synthetic
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                                                                                                                                                                                                                                                       This is Escherichia coll heat-labile toxin (LT) A subunit (LT-A) double mutant $63K+R192G. The wild-type serine was replaced with lysine at residue 53 and wild-type arguine was replaced with spine at residue 20 of the mature protein. The coding sequence contains plant-preferred codons and eliminates sequence motifs associated with spurious mRNA processing. A single codon insertion (GTG encoding valine) was made to accompact the creation of a NcoI restriction site around the initiator methionine codon. Novel polynucleotides encode a mutant IT-A polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A subunit (CT-A) collapspide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding IT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible vaccines, especially oral vaccines in transgenic plants for the production of plant cells for the production against E. coli or V. cholerae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 LSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPYSQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 IYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHA 183
                                                                                                                                                                                New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The mutant polypeptides are also useful as adjuvants.
Note: This sequence does not appear in the specification. It was constructed from the wild type LT-A shown in AAY96646 which is given in Figure 1 of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.1%; Score 125; DB 21; Length 259; 100.0%; Pred. No. 2.9e-120; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant-optimized E. coli LT-A R72 mutant.
                                                                           (BOYC-) BOYCE THOMPSON INST PLANT RES. (MASO/) MASON H S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY96649 standard; Protein; 259 AA.
                                                                                                                                                                                                                                    Example 5; Page -; 103pp; English.
                           99WO-US30747.
                                                   98US-0113507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 125; Conservative
                                                                                                                                Mason HS, Arntzen CJ;
                                                                                                      (ARNT/) ARNTZEN C J.
                                                                                                                                                         WPI; 2000-442653/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 PQGCG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pqgcg 207
                         22-DEC-1999;
                                                  22-DEC-1998;
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29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LT-A). The wild-type alanine was replaced with arginine at residue 72 of the mature protein, which was caused by a nucleotinde change of GC to AG at position 273-274 in the coding sequence. The sequence contains plant-preferred codons and eliminates sequence motifs associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 produce edible vaccines, especially oral vaccines in transgenic plants for the prophylactic or therapeutic treatment against E. coli or V. cholerae. The mutant polypeptides are also useful as adjuvants. Note: This sequence does not appear in the specification. It was constructed from the wild type LT-A shown in AAY96646 which is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is mutant A72R Escherichia coli heat-labile toxin (LT) A subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                      /label= A72R
/note= "Wild type alanine is replaced by arginine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQGCG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                          'label= signal_peptide
                                                                                                                               /label = mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BOYC-) BOYCE THOMPSON INST PLANT RES.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Page -; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0113507.
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Matches 116; Conservative
                                                                                         .259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mason HS, Arntzen CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARNT/) ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-442653/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MASON H S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA51545
                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                          WO200037609-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                         22-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                           29-JUN-2000.
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Key
Peptide
                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MASO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133
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The mutant polypeptides are also useful as adjuvants.

Note: This sequence does not appear in the specification. It was
                                                                                                                                                                                                                                Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral; adjuvant; anti-bacterial; A72R+R192G; double mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211
/label= R192G
/note= "the wild type arginine is replaced by glycine
at position 192 of the mature sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- A72R
/note- "the wild type alanine is replaced by glycine
at position 72 of the mature sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals
                                                                                                                                                                                         Plant-optimized E. coli LT-A A72R+R192G mutant.
                                                                                                                                                                                                                                                                                                                                                                    1..19
/label- signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                           label mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BOYC-) BOYCE THOMPSON INST PLANT RES. (MASO/) MASON H S. (ARNT/) ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                     AAY96651 standard; Protein; 259 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Page -; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US30747.
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                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mason HS, Arntzen CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-442653/38.
                                                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200037609-A2
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                                                                                                                                                    26-SEP-2000
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                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                              AAY96651;
                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                    RESULT 10
                                                     AAY96651
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This sequence represents a fragment of an Escherichia coll heat labile toxin subunit A (LT-A). This protein is used in a method resulting in a mutant LT-A protein which has the wild type Ala residue at position 72 changed to an Arg residue resulting in a toxin which retains its immunogenicity but is detoxified. Detoxification is defined in the specification as a reduction in toxicity relative to wild-type toxin, such that any residual toxicity is sufficiently low to allow use as an effective immunogenic composition in humans without significant side effective immunogenic composition in humans without significant side immunogenic compositions, optionally comprising an adjuvant and/or a second immunogenic antigen. Such compositions can be administered to prevent disease in a subject e.g. traveller's diarrhose in humans. The protein or compositions are aspecially administered as vaccines useful to prevent or treat infections by enterotoxigenic strain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heat labile toxin subunit A; LT-A; mutant; immunogen; detoxification; carrier; adjuvant; prevention; treatment; disease; diarrhoea; vaccine; infection; enterotoxic.
                                                                                                                                                                                                                                                                                                               73 GQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPYSQIYGWYRVNF 132
                                                                                                                                                                                                                                                                                                                                                   Gaps
constructed from the wild type LT-A shown in AAY96646 which is given in Figure 1 of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutated Escherichia coli heat labile toxin subunit A - is immunogenic and detoxified relative to wild-type, useful e.g. in vaccines against E. coli enterotoxigenic strains and as an adjuvant
                                                                                                                                                                                                                                                                                                                                                                                                                                         133 GVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQGCG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                        Length 259;
                                                                                                                                                                                        DB 21; I
5.3e-111;
                                                                                                                                                                                     48.3%; Score 116; DB
100.0%; Pred. No. 5.3
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1..241
/note= "partial sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW65074 standard; protein; 240 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E. coli LT-A protein fragment.
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                                                                                                                                                                                                                                                    Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glullani MM, Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-272223/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                   Similarity
                                                                                            259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9818928-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAY-1998,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW65074;
                                                                                            Sequence
                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW65074
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AAR44016;
                                                Sequence
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                                                                                                                                                                                                                                                                                                             AAR44016
   25 X 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a fragment of a mutant Escherichia coli heat labile toxin subunit A (LT-A) where the wild type Ala residue at position 72 is replaced by an Arg residue resulting in a toxin which cretains its immunogenicity but is detoxified. Detoxification is defined in the specification as a reduction in toxicity relative to wild-type toxin, such that any residual toxicity is sufficiently low to allow use as an effective immunogenic composition in humans without significant side effects. The protein can be combined with an acceptable carrier in immunogenic compositions, optionally comprising an adjuvant and/or a second immunogenic antigen. Such compositions can be administered to prevent/treat disease in a subject e.g. traveller's diarrhoea in humans. The protein or compositions are especially administered as vaccines cuseful to prevent or treat infections by enterotoxigenic strain of E. coli in mammals (especially humans).
                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       Heat labile, toxin subunit A; LT-A; mutant; immunogen; detoxification; carrier; adjuvant; prevention; treatment; disease; diarrhoea; vaccine; infection; enterotoxic.
                                                                                                            Gaps
                                                                                                                                        1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
                                                                                                                                                          Mutated Escherichia coli heat labile toxin subunit A - is immunogenic and detoxified relative to wild-type, useful e.g. in vaccines against E. coli enterotoxigenic strains and as an adjuvant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- A72R
/note= "Wild type Ala residue is replaced by Arg"
                                                                                                           ;
0
                                                                                                                                                                                                                      Length 240;
                                                                                                                                                                                                    STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQ 111
                                                                                                         Indels
                                                                                            Pred. No. 6.9e-106;
                                                                            DB 19;
                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          E. coli LT-A mutant A72R protein fragment.
                                                                            46.2%; Score 111;
 mammals (especially humans).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rappuoli R;
                                                                                                                                                                                                                                                                                                               AAW65075 standard; protein; 240 AA
                                                                            46.22,
100.08; Pic
0; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page -; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96GB-0022660.
                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                          Best Local Similarity 100.
Matches 111; Conservative
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                              240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHIR-) CHIRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-0CT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9818928-A1
                                                                                                                                                                                                                                                                                                                                                                           11-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAY-1998
E. coli in
                              Sequence
                                                                            Query Match
                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                               AAW65075
SXS
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NOTE: This sequence does not appear in the specification but has been constructed from the wild-type sequence represented in AAW65074.
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                   142 NREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEFWIHHAPQGCGNSSRTITGDTCNE 201
                                                                                                                                                                                                                                                                                                                                  /note= "corresponds to position 63 in cholera toxin A subunit; wild-type Ser is substituted by Lys to reduce toxicity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enterotoxigenic bacteria; vaccine; immunogenic detoxified LT-A; protomer A; site-directed mutagenesis; reduced toxicity; ADP-ribosyltransferase activity.
                                                                                                                                                                                                                                          ö
                                                                                                                                                                               Length 240;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.2%; Score 99; DB 19; 100.0%; Pred. No. 1.6e-93; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                   202 ETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rappuoli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Lys-63" E.coli heat labile toxin subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR44016 standard; Protein; 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91IT-0MI3513.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-DEC-1993 (first entry)
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hol W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-227320/28.
                                                                                                                                                                                                           Similarity
                                                                                    240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAQ51317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domenighini M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-DEC-1992;
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                                                                                                                                                                            Query Match
Best Local Simi
Matches 99;
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WPI; 1993-227320/28
                              Similarity
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                                                                                                                                                                                                                                                                                              Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ51319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domenighini M,
                  Query Match
Best Local Simi
Matches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                       31-DEC-1991;
                                                                                                                                                                                                             08-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                             WO9313202-A.
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                                                                                                                                                                                           AAR44018;
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                                                                                         103 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGY 162
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                      /note= "corresponds to position 97 in cholera toxin A subunit; wild-type Val is substituted by Lys to reduce toxicity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic detoxified mutant cholera toxin and heat labile toxin - useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                         detoxified LT-A;
toxicity;
                                                           ö
                                      Length 236;
                                                           Indels
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                                      35.8%; Score 86; DB 14; I
100.0%; Pred. No. 3.7e-80;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                        enterotoxigenic bacteria; vaccine; immunogenic protomer A; site-directed mutagenesis; reduced ADP-ribosyltransferase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rappuol1 .R;
                                                                                                                                                                                                                                                    "Lys-97" E.coli heat labile toxin subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                                                               ...r
Misc-difference 93
                                                                                                                    163 RLAGFPPDHQAWREEPWIHHAPQGCG 188
                                                                                                                                AAR44017 standard; Protein; 236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domenighini M, Hol W, Pizza M,
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                                                                                                                                                                                                                               08-DEC-1993 (first entry)
                                                          86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-227320/28.
                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 AA;
         236 AA;
                                                                                                                                                                                                                                                                                                                 coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAQ51318
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                                                                                                                                                                                                                                                                                                                Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUL-1993
                                                                                                                                                                                                            AAR44017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
         Sequence
                                       Query Match
                                                 Best Local
                                                         Matches
                                                                                                                                        159
                                                                                                                                                                                AAR44017
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                                                                                                                                       103 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGY 162
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "corresponds to position 97 in cholera toxin
A subunit; wild-type Val is substituted by
Tyr to reduce toxicity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enterotoxigenic bacteria; vaccine; immunogenic detoxified LT-A; protomer A; site-directed mutagenesis; reduced toxicity; ADP-ribosyltransferase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic detoxified mutant cholera toxin and heat labile to useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                      Length 236;
                                                                              Indels
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                      DB 14; I
3.7e-80;
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35.8%; Sco...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Tyr-97" E.coli heat labile toxin subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rappuoli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                           163 RLAGFPPDHQAWREEPWIHHAPQGCG 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hol W, Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR44018 standard; Protein; 236
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                                                                           Conservative
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        Query Match
        35.8%;
        Score 86;
        DB 14;
        Length 236;

        Best Local Similarity 100.0%;
        Pred. No. 3.7e-80;
        Ace 80;
        Ace 80;
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Search completed: June 10, 2002, 17:36:16 Job time: 223 sec

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J. Biol. Chem. 257, 5716-5721, 1982

A.Title: Escherichia coli heat-labile enterotoxin. Nucleotide sequence of the A subun A.Title: Escherichia coli heat-labile enterotoxin. Nucleotide sequence of the A subun A.Title: Escherichia coli heat-labile enterotoxin. Nucleotide sequence of the A subun A.Accession: A01817

A.Accession: A01817

A.Moria and A.Title: Bvolutionary origin of pathogenic determinants in enterotoxigenic Escherichia A.Accession: A26946; Muid:87137303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Escherichia coli

C; Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 17-Mar-1999

C; Accession: A61345

R; Spicer, E.K.; Kavanaugh, W.M.; Dallas, W.S.; Falkow, S.; Konigsberg, W.H.; Schafer,

Proc. Natl. Acad. Sci. U.S.A. 78, 50-54, 1981

A; Title: Sequence homologies between a subunits of Escherichia coli and Vibrio choler

A; Reference number: A61345; MUID:81223767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for residue 53
                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Mosaidues: 1-21, KR, 23-206, NV, 208-230, E', 232-255, 'D', 257-258 <XAM>A; Cross-references: EMBL: M15363 C; Comment: The heat-labile enterotoxin molecule contains one A chain and five or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 YGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEFWIHHAP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 YGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMINLYDHARGTQTGFVRYDDGYVSTSL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F:1.18/Domain: Signal sequence #status predicted <SIG>F:1-258/Product: heat-labile enterotoxin chain A #status predicted <WAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heat-labile enterotoxin A chain precursor - Escherichia coli (fragments)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              residue 27 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.7%; Score 184; DB 1; Lv
100.0%; Pred. No. 4.2e-190;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: eltA
C;Superfamily: heat-labile enterotoxin chain A
C;Keywords: enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Status: preliminary
A; Molecule type: DNA
A; Residues: 1-125 <SDN STACK
A; Crossidues: 1-125 <SDN STACK
A; Crossidues: CDN STACK
A; Crossidues: CDN STACK
A; Crossidues: CDN STACK
C; Superfamily: heat-labile enterotoxin chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 11.29
Best Local Similarity 100.
Matches 27; Conservative
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Matches 184;
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                                                                                                                                                        June 10, 2002, 17:33:24 ; Search time 19.04 Seconds (without alignments) 1211.210 Million cell updates/sec
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heat-labile entero
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C;Date: 30-Apr-1981 #sequence_revision 17-Oct-1997 #text_change 18-Jun-1999
C;Accession: 155231; A01811; A26946
C;Accession: 155231; A01817; A26946
J; Blol. Chem. 259, 5037-5044, 1984
A;Title: Primary structure of hat-labile enterotoxin produced by Escherichi
A;Reference number: 155231; MUID:84185610
A;Accession: 155231
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-258 <RES>
A;Residues: 1-258 <RES>
A;Cross-references: GB:K01995; NID:g148027; PIDN:AAA24685.1; PID:g148028
R;Spicer, E.K.; Noble, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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240
1 NGDRLYRADSRPPDEIKRSG.....QIFSDYQSEVDIYNRIRDEL
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Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                          283138 segs, 96089334 residues
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                           GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Listing first 45 summaries
                                                                                                                        sw model
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Gapop 60.0 , Gapext 60.0
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A61345
XVVCA
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T23104
T23103
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seq length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Match 1
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Maximum DB
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                                                                                                                                                                  Run on:
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No.
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as

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A;Status: preliminary
A;Notecule type: DNA
A;Motecule type: DNA
A;Residues: 1.258 <- AIEI>
A;Cross-references: GB:AE004224; GB:AE003852; NID:g9655952; PIDN:AAF94614.1; GSPDB:G
A;Experimental source: serogroup O1; strain NI6961; biotype El Tor
C;Genetics:
A;Gene: VC1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cholera enterotoxin chain A2 - Vibrio cholerae (serotype 0139)

N.Alternate names: CTA2 cholera toxin chain A2

S.Spacies: Vibrio cholerae

A.Variety: serotype 0139

C.Spacies: Vibrio cholerae

A.Variety: serotype 0139

C.Date: 08-May-1995 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999

C.Spacession: 539239, 539240

C.Spacession: 539239

A.Poscription: Structure and arrangement of the Cholera toxin genes in vibrio Cholera

A.Reference number: 539238

A.Accession: 539239

A.Acces
A; Molecule type: DNA
A; Residues: 1-6 <BAU>
A; Residues: 1-6 <BAU>
A; Residues: 1-6 <BAU>
A; Crossreferences: GB: MB3563; NID:g155314; PIDN: AAA27583.1; PID:g155316
A; Crossreference extracted from NCBI backbone (NCBIN:77488; NCBIP:77496)
R; Note: sequence extracted from NCBI backbone (NCBIN:77488; NCBIP:77496)
R; Heidelberg, J.E.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R-chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Seller I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID: 20406833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 1
C;Complex: the cholera enterotoxin molecule contains three kinds of chains; an alpha
ciate noncovalently with the subunit B, an aggregate of five beta chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: the acitive component of the toxin that is primarily responsible for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
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hes 0;
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D84514
dynamin-like protein [imported] - Arabidopsis thaliana
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ive 0; Mismatches
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100.0%; Pred. No. 0.0
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 EYFDRGTQMNINLYDHARGTQTGFVR 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.8 Best Local Similarity 100. Matches 26; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                C; Species: Vibrio cholerae
C; Species: Vibrio cholerae
C; Species: Vibrio cholerae
C; Species: Vibrio cholerae
C; Accession: A05129; S14623; S14625; A91268; A91286; A91746; A92298; S17665; B43864; A82
R; Maktanos, J.J.; Swartz, D.J.; Pearson, G.D.N.; Harford, N.; Groyne, F.; de Wilde, M.
R; Reference number: A93320; MUID:84068199
A; Rocession: A05129
A; Molecule type: DNA
A; Residues: 1-258 < MEX
B; Dams, E.; de Wolf, M.; Dierick, W.
Submitted to the EMBL Data Library, March 1991
A; Description: Correction of the cholera toxin nucleotide sequence of the Vibrio cholera
A; Reference number: S14623
A; Molecule type: DNA
A; Residues: 1-258 < CDA1>
A; Molecule type: DNA
A; Residues: 1-258 < CDA1>
A; Accession: S14623
A; Accession: S14623
A; Molecule type: DNA
A; Residues: 1-258 < CDA1>
A; Rocession: S14625
A; Coross-references: EMBL: X58786; NID:948420; PIDN:CAA41592.1; PID:948421
A; Residues: preliminary
A; Molecule type: DNA
A; Experimental source: strain 2125
A; Steperimental source: strain 2125
A; Steperimental source: strain 2125
A; Steperimental sources: Strain 2125
A; Steperimental sources: Strain 2125
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A; Residues: 37.38, 'L', 40.44, 'SE', 47-49, 'B', 51-55, 'B', 57, 'B', 59-60, 'B', 62-66, 'Z', 68-72,'
B; Duffyj L.K.; Peterson, J.W.; Kurosky, A.
FEBS Lett. 126, 187-190, 1981
A; Title: Isolation and characterization of a precursor form of the 'A' subunit of chole A; Reference number: A91286; MUID: 81212799
A; Reference number: A91286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule Type: DNA
A; Residues: 1-258 < DAA>
A; Residues: 1-258 < DAA>
A; Coss.references: EMBL:X58785; NID:948889; PIDN:CAA41590.1; PID:948889
A; Cross.references: Experimental source: strain 569B
B; Lai, C.Y.; Cancedda, F.; Chang, D.
FBBS Lett. 100, 85-89, 1979
A; Title: Primary structure of cholera toxin subunit A-1. Isolation, partial sequences A; Reference number: A91268; MUID:79169830
A; Reference number: A91268
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R;Baudry, B.; Fasano, A.; Ketley, J.; Kaper, J.B.
Infect. Immun. 60, 428-434, 1992
A;Title: Cloning of a gene (zot) encoding a new toxin produced by Vibrio cholerae.
A;Reference number: A43864; MUID:92112300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cholera enterotoxin chain A precursor VC1457 [validated] - Vibrio cholerae
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A:Residues: 213-246,'ID', 249-255,'N', 257-258
R:Dams, E.; de Wolf, M.; Dierick, W.
B:Damin. Biophys. Acta 1090, 139-141, 1991
A:Title: Nucleotide sequence analysis of the A:Reference number: 817665; MUID:91355224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-258 <DAM>
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A; Status: preliminary
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Length 1130 0; Indels

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A.Map position: 5
A.Introns: 71/2; 183/2; 339/1; 659/3; 699/1; 963/2; 998/3; 1080/3; 1105/1
                                                                                                        3.3%; Score 8; DB 2;
100.0%; Pred. No. 7.9;
iive 0; Mismatches
                                                                                                        Query Match 3.3
Best Local Similarity 100.
Matches 8; Conservative
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529 ERLHRNRE 536
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C.Species: African horse sickness virus
C.Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 07-May-1999
C.Accession: B44053
T.Natla. H.; Yamagawa, M.; Roy, P.
Virology 191, 251-261, 1992
A;Title: Evolutionary relationships among the gnat-transmitted orbiviruses that cause Af
                                                                       Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. Buss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
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A;Molecule type: DNA
A;Residues: 1-1130 <WIL>
A;Residues: 1-1130 <WIL>
A;Cross-references: EMBL:292835; PIDN:CAB07397.1; GSPDB:GN00023; CESP:H19N07.2b
A;Experimental source: Clone H19N07
C;Genetics:
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C;Species: Caenorhabditis elegans
C;Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21104
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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100.0%; Pred. No. 5.6;
iive 0; Mismatches
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100.0%; Pred. No. 6.5;
tive 0; Mismatches
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A; Residues: 1-905 < TINA>
A; Cross-references: GB: M94681
C; Superfamily: bluetongue virus core protein VP3
C; Keywords: capsid protein
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A;Accession: B44053
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Best Local Similarity 100.
Matches 8; Conservative
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Matches 8; Conservative
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A;Molecule type: DNA
A;Residues: 1-782 <STO>
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791 DSRPPDEI 798
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A;Gene: CESP:H19N07.2b
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A;Map position: 2
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hypothetical protein H19N07.2a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T23103
R;Dobson, R:
Submitted to the EMBL Data Library, March 1997
A;Reference number: 219678
A;Reference number: 219678
A;Accession: T23103
A;Accession: T2310
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A;Map position: 5
A;Introns: 71/2; 183/2; 339/1; 659/3; 699/1; 963/2; 1001/3; 1083/3; 1108/1
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100.0%; Pred. No. 7.9;
ive 0; Mismatches
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Matches 8; Conservative
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FROM N.A.
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(without alignments)
841.729 Million cell updates/sec
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P01555 vibrio chol
P43528 escherichia
P32509 african hor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ISOLATE P307;
MEDIJINE-87137303; Pubmed-3546573;
Yamamoto T., Gojobori T., Yokota T.;
"Evolutionary origin of pathogenic determinants in enterotoxigenic Escherichia coli and Vibrio cholerae 01.";
J. Bacteriol. 169:1352-1357(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELAP_ECOLI STANDARD; PRT; 258 AA.
P06717; P01554;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Heat-labile enterotoxin A chain precursor (LT-A, porcine) (LTP-A).
                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                        .....QIFSDYQSEVDIYNRIRDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                               June 10, 2002, 17:36:39; Search time 11.04 Seconds
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                      105224 seqs, 38719550 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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ELAH_ECOLI
CHTA_VIBCH
E2BA_ECOLI
VP3_AHSV4
                                             OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Crystal structure of a cholera toxin-related heat-labile enterotoxin from E. coli.";
Nature 351:371-377(1991).
                                                                                                                                                                                                                                                                                                   Spicer E.K., Noble J.A.; "Escherichia coli heat-labile enterotoxin. Nucleotide sequence of the
STRAIN=ISOLATE P307;

Dykes C.W., Halliday I.J., Hobden A.N., Read M.J., Harford S.;

Dykes C.W. and Index I.J., Hobden A.N., Read M.J., Harford S.;

A comparison of the nucleotide sequence of the A subunit of heat-
labile enteriorxin and cholera toxin.";

FEMS Microbiol. Lett. 26:171-174(1985).
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BDLINE-9128966; PubMed-2034287;
Sixma T.K., Pronk S.E., Kalk K.H., Wartna E.S., van Zanten B.A.M.,
Witholt B., Hol W.G.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tsuji T., Inoue T., Miyama A., Okamoto K., Honda T., Miwatani T.; As single amino acid substitution in the A subunit of Escherichia coli enterctoxin results in a loss of its toxic activity."; J. Biol. Chem. 265:22520-22525(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
MEDLINE-923240541; PubMed-6478941;
Sixma T.K., van Zanten B.A.M., Dauter Z., Hol W.G.J.;
"Refined structure of Escherichia coli heat-labile enterotoxin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-40 FROM N.A.
Trachman J.D., Maas W.K.;
Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 257:5716-5721(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               close relative of cholera toxin."; J. Mol. Biol. 230:890-918(1993).
                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ISOLATE P307;
MEDLINE-82167425; Pubmed-6279611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-ISOLATE P307;
MEDLINE-91093102; Pubmed-2266142;
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EMBL; M61015; AAA24335.1;
EMBL; A04913; CAA00402.1;
PIR, A26946; OLECEA.
PIR; A01817; QLECA.
PDB; LLTB; 31-JAN '94.
PDB; 1LTB; 31-JUL-94.
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YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI

258 AA

PRT;

STANDARD;

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SECUENCE FROM N.A.
STRAIN=ISOLATE H10407;
MEDLINE=84185610; PubMed=6325417;
Yamamoto T., Tamura T., Yokota T.;
"Primary structure of heat-labile enterotoxin produced by Escherichia coli pathogenic for humans.";
J. Biol. Chem. 259:5037-5044(1984).
                                                                                   181 HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL
                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Heat-labile enterotoxin A chain precursor (LT-A, human) (LTH-A).
ELTA OR LTPA OR TOXA.
                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacterlaceae;
Escherichia.
                                                                                                                                                                                                                                                Escherichia coli.
                                                                                                                                                                                                                                                                                NCBI_TaxID=562;
                                                                                                                                                                 ELAH_ECOLI
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                                                                                                                                                      ELAH_ECOLI
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                                                                                                                                                            E -> K (IN INACTIVE MUTANT).
SGG -> FRS (IN REF. 3).
MISSING (IN REF. 3).
S -> Y (IN REF. 3).
TYXIXVIATAP -> LTIXIVIA (IN REF. 3).
LG -> IS (IN REF. 3).
R -> G (IN REF. 4).
N -> D (IN REF. 3).
                                                                                                                            HEAT-LABILE ENTEROTOXIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2F0786442619F81F CRC64;
                                                               Pfam; PF01375; Enterotoxin_A. Pfam; PF01375; Enterotoxin_A; 1. PRINTS; PR00771; ENTEROTOXINA.
                                                                                                     Enterotoxin; Signal; 3D-structure.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29902 MW;
                                                                                                                193
200
204
                      31-JAN-94.
07-JUL-97.
16-JUN-97.
20-APR-95.
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242
250
258 AA;
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                       1LTT;
                                   PDB; 1LT3;
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VARIANT
CONFLICT
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIR-ISOLARE H10407;
STRAIR-ISOLARE H10407;
MEDLINE-93252225; Pubhed-8486242;
Inoue T., Tsuji T., Koto M., Imamura S., Miyama A.;
"Amino acid sequence of heat-labile enterotoxin from chicken enterotoxigenic Escherichia coli is identical to that of human strain H 10407.";
STRAIN-ISOLATE #10407;
MEDLINE-SOLATE #10407;
Yamamocto T., Gojobori T., Yokota T.;
"Evolutionary origin of pathogenic determinants in enterotoxigenic Escherichia coli and Vibrio cholerae 01.";

"Bacteriol. 169:1352-1357(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISCUSSION OF SEQUENCE.

MEDLINE-95349400; PubMed-7623669;

Domenighini M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli R.;

Identification of errors among database sequence entries and
comparison of correct amino acid sequences for the heat-labile
enterotoxins of Escherichia coli and Vibrio cholerae.";

Mol. Microbiol. 15:1165-1167(1995).

- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED BY
THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENIL CYCLASE.

- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEMS Microbiol. Lett. 108:157-161(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; K01995; AAA24685.1; -. EMBL; S60731; CAB31891.1; -. HSSP; P06717; 1LTG.
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Gaps

0;

Length 258; 0; Indels

Query Match 100.0%; Score 240; DB 1; I Best Local Similarity 100.0%; Pred. No. 2.7e-249; Matches 240; Conservative 0; Mismatches 0;

STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120

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Submitted (MAY-1991)
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STRAIN-CLASSICAL 569B / ATCC 25870 / SEROTYPE 01;
MEDLINE-91355224; PubMed-1883840;
Dams E., de Wolf M., Dierick W.;
"Nucleotide sequence analysis of the CT operon of the Vibrio cholerae
                                                                                                                                                                                                                     143 YGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAP 202
                                                                                                                                                                                                                                                   125 YGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAP 184
                                                                                                                                                                                                            SLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPYSQI 124
                                                                                                                                                 Gaps
                                                                                                                                                                  64
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STRAIN=EL TOR 2125;
MEDLINE-84068199; PubMed-6646234;
Mekalanos J.J., Swartz D.J., Pearson G.D.N., Harford N., Groyne F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-1854 / 0139-BENGAL;
Yamamoto K., Do V.G.R.F., Xu M., Iida T., Miwatani T., Albert M.J.,
                                                                                                                                                                             23 LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSL
                                                                                                                                                                                                                                                                                                                                                                CHTA_VIBCH STANDARD; PRT; 258 AA.
CHTA_VIBCH STANDARD;
21-JUL-1986 (Rel. 01, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2011 (Rel. 40, Last annotation update)
17-Dosyltransferase) (EC 2.4.2.36) (Cholera enterotoxin, A chain precursor (NAD(+)--diphthamide ADP-ribosyltransferase) (EC 2.4.2.36) (Cholera enterotoxin A subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                   LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 de Wilde M.; "Cholera toxin genes: nucleotide sequence, deletion analysis and
                                                                                                                                                ö
                                                   HEAT-LABILE ENTEROTOXIN A CHAIN.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                         86.7%; Score 208; DB 1; Length 258; llarity 100.0%; Pred. No. 5e-215; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases
                                                                                 N -> D (IN REF. 1 AND 3).
2BB153C777FD78B7 CRC64;
                                          SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        classical strain 569B.";
Biochim. Biophys. Acta 1090:139-141(1991).
                                                                                                                                                                                                                                                                                                       203 QGCGNSSRTITGDTCNEETQNLSTIYLR 230
                                                                                                                                                                                                                                                                                            185 QGCGNSSRTITGDTCNEETQNLSTIYLR 212
InterPro; IPR001144; Enterotoxin_A. Pfam; PF01375; Enterotoxin_A; 1. PRINTS; PR00771; ENTEROTOXINA.
                                                                                             MM:
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STRAIN-EL TOR 2125;
Dams E., de Wolf M., Dierick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine development.";
Nature 306:551-557(1983).
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128
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258 AA;
                                Enterotoxin; Signal
                                                                                                                                   Best Local Similarity
Matches 208; Conserv
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X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
MEDLINE=95387395; PubMed=7658473;
Zhang R.G., Scott D.L., Westbrook M.L., Nance S., Spangler B.D.,
Shipley G.G., Westbrook E.M.;
"The three-dimensional crystal structure of cholera toxin.";
J. Mol. Biol. 251:563-573(1995).
-1- FUNCTION: THE ALPHA/GAMMA CHAIN (A SUBUNIT) IS AN ADP-RIBOSYLATING
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-20406833; PubMed-10952301;

MEDLINE-20406833; PubMed-10952301;

Medidelberg J.F., Eisen J.A., Nack, C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Ummyam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vammathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-212 FROM N.A.
STRAIN-CLASSICAL, 569B / ATCC 25870 / SEROTYPE 01;
MEDLINE-85006737; Pubbed-6090390;
Lockman H.A., Galen J.E., Kaper J.B.;
"Vibric cholerae enterotoxin genes: nucleotide sequence analysis of DNA encoding ADP-ribosyltransferaes.";
J. Bacteriol. 159:1086-1089(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE-79169830; PubMed-437113;
Lai C.-Y., Cancedda F., Chang D.;
Primary structure of cholera toxin subunit Al: isolation, partial
sequences and alignment of the BrCN fragments.";
FEBS Lett. 100:85-89(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-82053094; PubMed-7028752;
Duffy L.K., Peterson J.W., Kurosky A.;
"Covalent structure of the gamma chain of the A subunit of cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the three
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                      gene
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                                                                                                  STRAIN=KNIH002;
Shin H.J., Park Y.C., Kim Y.C.;
Cloning and nucleotide sequence analysis of the virulence (cassette from Vibrio cholerae KNIH002 isolated in Korea.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
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the EMBL/GenBank/DDBJ databases
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MEDLINE-81212799; PubMed-7238869;
Duffy L.K., Peterson J.W., Kurosky A.;
"Isolation and characterization of a precursor form of subunit of cholera toxin.";
FEBS Lett. 126:187-190(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Submort Structure and N-terminal amino acid sequence chains of choice and N-terminal amino acid sequence chains of choice and sequence chains of choice anteroccain.";
Immunochemistry 13:605-611(1976).
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MEDLINE-84061784; PubMed-6315707;
Lockman H., Kaper J.B.;
"Nucleotide sequence analysis of the A2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cholerae enterotoxin.";
J. Biol. Chem. 258:13722-13726(1983).
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MEDLINE-76259136; PubMed-955672;
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SEQUENCE OF 27-72 AND 111-139.
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                                                                        SEQUENCE FROM N.A.
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EMBL; EMBL;

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                                                                                                                    MEDINE-89359131; PubMed-2670900; Pickett C.L., Twiddy E.M., Coker C., Holmes R.K.; Pickett C.L., Twiddy E.M., Coker C., Holmes R.K.; "Clooning, mucleotide sequence, and hybridization studies of the type IIIb heat-labile enterotoxin gene of Escherichia coli."; J. Bacteriol. 171:4945-4952(1989).
                                                                                                                                                                                                                                              MEDLINE-96399713; PubMed-8805549;
van den Akker F., Sarfaty S., Twiddy E.M., Connell T.D., Holmes R.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       African horse sickness virus 4 (AHSV-4) (African horse sickness virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Iwata H., Yamagawa M., Roy P.;
"Evolutionary relationships among the gnat-transmitted orbiviruses
that cause African horse sickness, bluetongue, and epizootic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEAT-LABILE ENTEROTOXIN IIB, A CHAIN.
                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                "Crystal structure of a new heat-labile enterotoxin, LT-IID.";
Structure 4:665-678(1996).
-!- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED
THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
-!- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.6%; Score 11; DB 1; Length 263;
100.0%; Pred. No. 0.0005;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (serotype 4)).
Viruses; dsRNA viruses; Reoviridae; Orbivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 905 AA. P32509; 064923; 01-0CT-1993 (Rel. 27, Created) 15-DEC-1998 (Rel. 37, Last sequence update) VP3 core protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. No. 0.C
Live 0; Mismatches
                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDB; 1TII; PRELIMINARY.
INTERPRO; IPRO01144; ENTEROTOXIn_A.
PFEm; PF01375; ENTEROTOXIn_A; 1.
PRINTS; PR00771; ENTEROTOXINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterotoxin; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93033117; PubMed-1329319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M28523; AAA53285.1; -.
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Matches 11; Conservative
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263 AA;
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                                                                                                       STRAIN-ISOLATE 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=36421;
 Escherichia coli
                                                  NCBI_TaxID=562;
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         CATALYTIC ACTIVITY: NAD(+) + peptide diphthamide = nicotinamide + peptide N-(ADP-D-ribosyl)diphthamide.
SUBUNIT: CONTAINS 3 KINDS OF CHAINS. AN ALPHA AND A GAMMA CHAIN (FROM THE SAME PRECURESON MOLECULE), LINKED BY AN INTERCHAIN DISULFIDE BOND, ASSOCIATE NONCOVALENTLY WITH AN AGGREGATE OF 4 TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERCHAIN (WITH GAMMA CHAIN).
INTERACT WITH NAD (BY SIMILARITY).
BY SIMILARITY.
D -> N (IN REF. 9).
S -> R (IN REF. 10).
G -> L (IN REF. 11).
QS -> SE (IN REF. 11).
N -> L (IN REF. 11).
S -> A (IN REF. 11).
M -> I (IN REF. 11).
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Fafain, PR01375; Enterotoxin_A; 1.
PRINTS; PR00771; ENTEROTOXINA.
Enterotoxin; Signal; NAD; Transferase; Glycosyltransferase;
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(Rel. 32, Last sequence update)
(Rel. 34, Last annotation update)
enterotoxin IIB, A chain precursor (LT-IIB).
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-> N (IN REF. 12).
0F7EBAE62069A5D0 CRC64;
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                                                                                                                                                                                                                                                                                                                                             29335 MW;
                                                                                                                                                                                                                                                                                                X58785; CAA41590.1; ... D30053; BAA06290.1; ... X58786; CAA41592.1; ... K02679; AAA27514.1; ...
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Matches 26; Conserva
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258 AA;
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01-NOV-1995 (
01-OCT-1996 (
Heat-labile e
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P43528;
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Viruses; dsRNA viruses; Reoviridae; Orbivirus.

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LITVNPTF -> IANLQANMGQFRAAIRRTLDDNGWIQFGG
MLRNIKIKFFDSRPPDEILT (IN REF. 1).
hemorrhagic disease as evidenced by their capsid protein sequences."; Virology 191:251-261(1992).
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                                                                                                           I -> V (IN REF. 1).
Q -> P (IN REF. 1).
Q -> P (IN REF. 1).
RALSDY -> ARET. 1).
BPOTGRGYNGW -> THKRVGLQRV (IN REF. 2).
F -> L (IN REF. 1).
F -> T (IN REF. 1).
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I -> V (IN REF. 1).
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100.0%; Pred. No. 2.5;
ive 0; Mismatches
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R -> A (IN REF.
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EMBL; D26572; BAA05621.1; --
PIR; B44053; P3XRA4
HSSP; P56582; ZBTV.
                                                                                           MEDLINE-94270993; PubMed-8002793;
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Pfam; PF01700; Orbi_VP3; 1.
ProDom; PD004438; Orbi_VP3; 1.
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Matches 8; Conservative
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905 AA;
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                                                             SEQUENCE FROM N.A.
MEDILINE-9872831; PubMed-9617769;
MEDILINE-9872831; PubMed-9617769;
MILITARS C.F., Inoue T., Lucus A.-M., Zanotto P., Roy P.;
"The complete sequence of four major structural proteins of African horses sickness virus serotype 6: evolutionary relationships within and between the orbitituses.";
Virus Res. 53:53-73(1998).
--- FOWTION: THE VP3 PROTEIN IS ONE OF THE FIVE PROTEINS (WITH VP1, VP4, VP6 AND VP7) WHICH FORM THE INNER CAPSID OF THE VIRUS.
--- SIMILARITY: BELONGS TO THE REOVIRUSES VP3 FAMILY.
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Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches
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HSSP; P56582; 2BTV.
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DSRPPDEI 798
NCBI_TaxID=86060;
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SEQUENCE 90
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Perfect score:

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Sequence:

Scoring table:

Word size

Searched:

Database :

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83 SLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPYSQI 142
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                                                                                                   LTH A SUBBNIT.
Escherichia coli.
Bacteriai, Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
NCBI_TaxID-562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ENTEROTOXIN A (FRAGMENT).
ESCRETICHIA COli.
ESCRETICHIA : Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
NCBI_TAXID=562;
                                                                                                                                                                                                                           Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                               01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-LABILE ENTENOTOXIN A SUBUNIT.
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                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-1032 (ENTEROTOXIGENIC);
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Best Local Similarity 100.
Matches 191; Conservative
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                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                      June 10, 2002, 17:36:19; Search time 26.46 Seconds (without alignments) 1569.115 Million cell updates/sec
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045623 caenorhabdi
09j599 fowlpox vir
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057372 vibrio chol
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1 NGDRLYRADSRPPDEIKRSG......QIFSDYQSEVDIYNRIRDEL 240
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                               OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Q47182
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045623
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sp_unclassified:*
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sp_invertebrate:*
sp_mammal:*
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sp_phage:*
sp_plant:*
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"Overlapping genes in the heat-labile enterotoxin operon originating
from Escherichia coli human strain.";
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"Sequence of heat-lablle enterotoxin of Escherichia coli pathogenic
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NCBL_TaxID=666;
                                                                   Yamamoto T., Tamura T., Ryoji M., Kaji A., Yokota T., Takano T.; Sequence analysis of the jeat-labile enterotoxin subunit B gene originating in human enterotoxigenic Escherichia coli."; J. Bacteriol. 152:506-509(1982).
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"Structure and arrangement of the cholera toxin genes in Vibrio cholerae 0.39";
FEMS Microbiol. Lett. 117:197-202(1994).
EMBL: X76391; CAA53975.1;
EMBL: X76391; CAA53976.1;
HSSP; P01555; 1XTC.
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InterPro; IPR000886; ER_target.
Pfam; PF01375; Enterotoxin_A; I.
PROSITE; PS00014; ER_TARGET: UNKNOWN_I.
SEQUENCE 46 AA; 5447 MW; IB6085A02E8889D6 CRC64; A
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Pred. No. 1.2e-16;
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100.0%; Pred. No. 1...
0; Mismatches
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InterPro; IPR000886; ER.target.
Pfam; PF01375; Enterotoxin_A; 1.
PRINTS; PR00771; ENTEROTOXINA.
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                                                                                                                                                                                                      STRAIN=H10407;
MEDLINE=83114628; PubMed=6759877;
                                            MEDLINE=83007048; PubMed=6749816;
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Bacteriol. 155:728-733(1983).
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17,
SEQUENCE OF 64-68 FROM N.A. STRAIN-H10407;
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HSSP; P06717; 1LT3.
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Best Local Similarity 100.
Matches 24; Conservative
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Mewes H.-W., Frishman D., Stocker S., Lupas A.M., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma
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Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
Thermoplasma.
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Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
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    Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acidophilum.";
Nature 407:508-513(2000).
EMBL: AL445066; CAC12122.1; -.
SEQUENCE 309 AA; 33633 WW; C39F9882B276B380 CRC64;
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                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL MEMBRANE PROTEIN
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  3.8%; Score 9; DB 2; 00.0%; Pred. No. 0.17;
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Best Local Similarity 100.0%; Pred. No. 9.5
Matches 8; Conservative 0; Mismatches
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01-0CT-2001 (TrEMBLrel. 18, Last seq
01-0CT-2001 (TrEMBLrel. 18, Last anno
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STRAIN-GSS1 / DSM 4299 / JCM 9571;
MEDLINE-20570466; PubMed=11121031;
                      100.08;
                                               9; Conservative
                                                                                                                                                                                                                                                             PRELIMINARY;
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Best Local Similarity
Matches 9: Constitution
                                                                                            213 EYQSKVKRQ 221
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
[1]
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Alonso J.L., Martinez J.L., Casal J.L.;
"Nucleoride sequence of the African horsesickness virus L3 gene.";
Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; M94312; AAA42542.1; -.
HSSP; P56582; 2BTV.
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                                                                             Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
REMEL; ACO7197; AAD5856.1; -
InterPro; IPR001401; Dynamin.
R InterPro; IPR003135; Dynamin_central.
R InterPro; IPR003130; GED.
R Pfam; PF00350; dynamin; 1.
R Pfam; PF01031; dynamin; 1.
R Pfam; PF0212; GED; 1.
R RANRT; SM00195; DYNAMIN.
R SMART; SM00053; GED; 1.
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Pfam; PF01700; Orbi_VP3; 1.
ProDom; PD004438; Orbi_VP3; 1.
SEQUENCE 903 AA; 102980 MW; B261DAEF08EA42AA CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1NDER SHELL PROFEIN.
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Last annotation update)
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NCBI_TaxID=10896;
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100.0%; Pred. No. ...
0; Mismatches
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045624;
01-JUN-1998 (TrEMBLEE]. 06, C3
01-JUN-1998 (TrEMBLEE]. 06, L6
01-DEC-2001 (TrEMBLEE]. 19, L6
H19N07.2B PROTEIN.
H29N07.2B.
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Best Local Similarity 100.،
المالية 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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                               STRAIN-CV. COLUMBIA;
Lin X.;
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Q64928;
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SETAINE-20083487; PubMed-10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujil C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAen S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Salzberg S.L., Fraser C.M., Venter J.C., White O., Eisen J.A.,
Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                         Gaps
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NCBI_TaxID=10261;
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                               Length 330;
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STRAIN-TCP-BLEN (CEVA);
Stefancs1k R., Rauch T.;
Fowlpox virus TCP-BLEN (CEVA).";
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U17141; AAB40513.1;
InterPro; IPR000209; Peptidase_S8.
PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1.
                                                                                      Indels
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SEQUENCE 616 AA; 68545 MW; 3177A67B8520B24A CRC64;
                                                                                                                                                                                                                                                                                                                                                    P87708; (TEMBLrel. 03, Created) 01-MAY-1997 (TEMBLrel. 03, Last sequence update) 01-MAY-1997 (TEMBLrel. 03, Last sequence update) 01-DEC-2001 (TEMBLrel. 19, Last annotation update) ORF1 AND ORF2 GENES, ORF3 AND ORF4 GENES (FRAGMENT).
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Last sequence update)
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                         3.3%; Score 8; DB 17;
100.0%; Pred. No. 10;
ative 0; Mismatches
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100.0%; Pred. No. 18;
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Best Local Similarity 100.00
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                                                                                   Conservative
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SEQUENCE FROM N.A.
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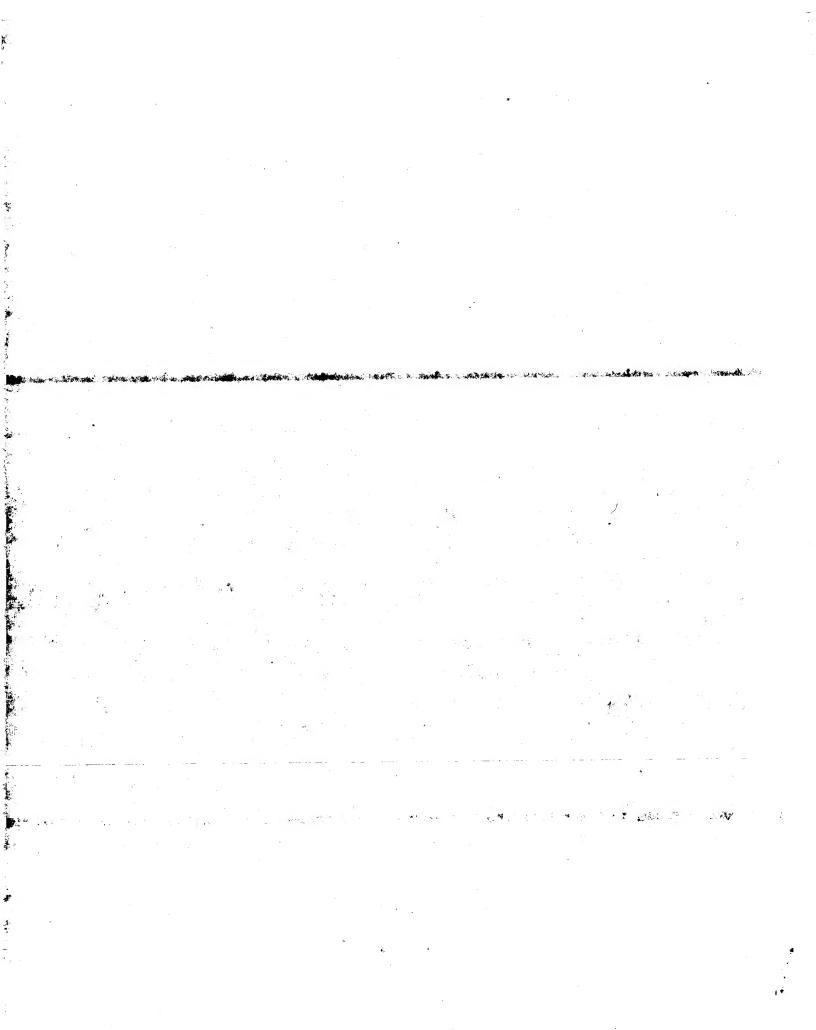
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Gaps

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Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
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InterPro; IPRO1306; Ig_MHC.
InterPro; IPRO1306; MATH.
InterPro; IPRO1304; UCH-2.
InterPro; IPRO0413; UCH-2.
InterPro; IPRO0443; UCH-1; 1.
InterPro; IPRO0443; UCH-1; 1.
InterPro; IPRO0443; UCH-2.
IPRO0444; UCH-2.
IPRO0444; UCH-2.
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IPRO0444; UCH-2.
IPRO0444; UCH-2.
IPRO04
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RICHEPPO; IPRO03006; Ig_MHC.
RICHEPPO; IPRO01039; MATH.
RICHEPPO; IPRO0134; UCH-2.
R Pfam; PF00442; UCH-1: 1.
R Pfam; PF00443; UCH-2: 1.
R PROSITE; PS00290; IG_MHC; UNKUNW_1.
R PROSITE; PS00390; IG_MCH; 1.
R PROSITE; PS00393; UCH_2_1: 1.
R PROSITE; PS00395; UCH_2_2: 1.
                                                                                                                                                                                                                                                                            "Genome sequence of the nematode C.elegans: A platform for investigating biology."; science 282:2012-2018(1998). EMBL: 292835; C19.UPW; -. MEROPS; C19.UPW; -.
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EMBL: 292835; CAB07396.1; -.
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100.0%; Pred. No. 32;
iive 0; Mismatches
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MEDLINE-99069613; Pubmed-9351916;
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MEDLINE-99069613; Pubmed-9851916;
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045623;
01-JUN-1998 (TrEMBLrel. 06, C:
01-JUN-1998 (TrEMBLrel. 06, L:
01-DEC-2001 (TrEMBLrel. 19, L:
H19N07.2A PROTEIN.
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Matches 8; Conservative
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SEQUENCE FROM N.A.
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MEDLINE=20193820; PubMed=10729156;
Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
"The genome of fowlpox virus.";
J. Virol. 74:3815-3831(2000).
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EMBL, AF198100; AAF44467.1; -.
InterPro; IPR000209; Peritalse_S.B.
PROSTIE; PS00136; SUPFILAISE_ASP; UNKNOWN_1.
SEQUENCE 1766 AA; 201146 MW; B3DB7FF4452679D9 CRC64;
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                    Length 1133;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ORF FPV123 VARIOLA B22R GENE FAMILY PROTEIN.
FPV123.
                      DB 5;
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                  3.3%; Score 8; DB 5
100.0%; Pred. No. 32;
tive 0; Mismatches
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100.0%; Pred. No. 48;
ive 0; Mismatches
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Query Match
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Best Local 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                      137 ERLHRNRE 144
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Sequence 8, Appli Sequence 2, Appli Sequence 2, Appli Sequence 10, Appl Sequence 11, Appl Sequence 7, Appli Sequence 8, Appli

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GENERAL INFORMATION:
APPLICANT: Domenighini, Mario
APPLICANT: Rano
APPLICANT: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
APPLICANT: Respuoli, Rino
APPLICANT: Respuoli, Rino
APPLICANT: Pizza, Mariagrazia
TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Preparation and
TITLE OF INVENTION: Their Use for the Preparation of Vaccines
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 188; DB 4; Length 240;
Pred. No. 1.8e-181;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,120
FILING DATE:
US-08-823-120-8
US-08-449-045C-2
US-08-435-605A-2
5236L0-2
US-08-435-605A-49
US-08-296-848A-2
US-08-292-968-7
US-08-292-968-7
US-08-467-974-7
US-08-467-974-7
US-08-467-974-7
US-08-467-974-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MCClung, Barbara G.
REGISTRATION NUMBER: 33,113
REELENCKPLOCKET NUMBER: 0315.001
TELEPHONE: (510) 601-2708
TELEPHONE: (510) 601-2708
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,003
FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 3, Application US/08823120
; Patent No. 6149919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.3%; S
100.0%;
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STREET: 4560 Horton Street
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: amino acid
STRANDEDNESS: single
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California
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US-08-823-120-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-823-120-3
    Sequence 114, App
Sequence 57, Appl
Sequence 6, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 50, Appl
Sequence 51, Appl
                                                                                                                                    June 10, 2002, 17:33:09; Search time 13.05 Seconds (without alignments) 449.206 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, App
Sequence 114, P
Sequence 124, P
                                                                                                                                                                                                                    US-09-297-171-1
240
1 NGDRLYRADSRPPDEIKRSG.....QIFSDYQSEVDIYNRIRDEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                       GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-823-120-6
US-08-846-099-114
US-08-186-0107A-124
US-08-186-114
US-08-18-551A-114
US-08-485-551A-114
US-08-485-551A-114
US-08-485-565A-114
US-08-435-665A-8
US-08-435-665A-8
US-08-435-665A-14
US-08-435-665A-14
US-08-435-665A-14
US-08-435-665A-14
US-08-435-665A-15
US-08-435-665A-50
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US-08-435-605A-52
US-08-435-605A-53
US-08-435-605A-56
US-08-823-120-4
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                                                                                                                                                                                                                                                                                                                                                                 231628 segs, 24425594 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Listing first 45 summaries
                                                                                                  - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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                                                                                                  OM protein
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                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                          Run on:
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No.
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163 RLAGFPPDHQAWREEPWIHHAPQGCG 188
                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-486-099-114
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
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                                                                                                                                US-08-486-099-114
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                                                                                                           61 STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                               121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                      103 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGY 162
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                                    1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Domenighini, Mario
APPLICANT: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
TITLE OF INVENTION: Immunogenic Detoxifled Mutants of
TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Prepartite OF INVENTION: Their Use for the Preparation of Vaccines
TITLE OF INVENTION: Their Use for the Preparation of Vaccines
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
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     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,120
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0
 0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,003
FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0315.001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-08-823-120-6
; Sequence 6, Application US/08823120
; Patent No. 6149919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (510 (655 3542)
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-823-120-6
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94608-2916
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APPLICANT: Domenio
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nes 86; Conserv
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Best Local Si
Matches 86;
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APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphons J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FORSON ASSOCIATED EVENTS, INCLUDING HEPATITIS
TITLE OF INVENTION: B VIRUS TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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8.3e-79;
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Pred. No.
                                                                                                                                                                                                                                                                                              E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07 V V VS/08/486,099 O7-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7872-031
Sequence 114, Application US/08486099
Patent No. 6013263
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 RLAGFPPDHQAWREEPWIHHAPQGCG 188
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4.08-08-36-107A-124

; Sequence 124, Application US/08360107A

; Patent No. 6017536
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100.0%; Pre
0; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 787
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 869-9741/886.
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 100.
Matches 86; Conservative
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Sequence 114, Application US/08919597
Patent No. 6054265
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Matthews, Thomas J.
APPLICANT: Mild, Carl T.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lampert, Dennis M.
APPLICANT: Lampelois, Alphonse J.
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV MIMADE OF EVENTS, INCLUDING HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 86; DB 3; Length 254;
Pred. No. 8.3e-79;
0; Mismatches 0; Indels
                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASSIFICATION 1945
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAULR A.
RECESTRATION NUMBER: 30,742
REFERENCY/DOCKEY NUMBER: 30,742
REFERENCY/DOCKEY NUMBER: 30,742
REFERENCY/DOCKEY NUMBER: 30,742
REFERENCY (212) 790-9090
TELECOMMUNICATION INFORMATION:
TELEFAN: (212) 786-971/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
TEMMINE 254 amino acids
TITLE OF INVENTION: TRANSMISSION NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
CARDESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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100.0%; Pre
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Best Local Similarity 100.
Matches 86; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & 1
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COMPUTER READABLE FORM:
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COMPUTER READABLE FORM:
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                                                                                                                                                New York
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                                                                                             STREET: 1155 AV
CITY: New York
STATE: New YOrk
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                                                                                                                                                                   USA
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                                                                                 APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Detteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dannis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGY 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 35.8%; Score 86; DB 3; L
Best Local Similarity 100.0%; Pred. No. 8.3e-79;
Matches 86; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                  E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 114, Application US/08484223B
Patent No. 6020459
GENERAL IMPORMATION:
APPLICANT: Bolognesi, Dani P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 790-9990
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENUE
INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
                        Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & 1
                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                        STREET: 1155 Ave
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                     New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-484-223B-114
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APPLICANT: Barney, Shawn O.
APPLICANT: Landbert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                     103 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                  35.8%; Score 86; DB.3; L
100.0%; Pred. No. 8.3e-79;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
        REFERENCE/DOCKET NUMBER: 7872-026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERBNCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 114, Application US/08485551A Patent No. 6068973 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 RLAGFPPDHQAWREEPWIHHAPQGCG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 RLAGFPPDHQAWREEPWIHHAPQGCG 202
                                               TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bolognesi, Dani P. APPLICANT: Matthews, Thomas J. APPLICANT: Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (212) 790-9090
(212) 869-9741/8864
                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-475-668A-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS
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TELEFAX: (
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| US-08-475-668A-114 |
| Sequence 114, Application US/08475668A |
| Patent No. 6060065 |
| Patent No. 6060065 |
| APPLICANT: Lambert, Dennis M. |
| APPLICANT: Lambert, Dennis M. |
| APPLICANT: Petteway, Stephen R. |
| TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE |
| TITLE OF INVENTION: TRANSMISSION |
| NUMBER OF SEQUENCES: 21 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Pennie & Edmonde II. |
| STREET: 1155 *****
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 86; DB 3; Length 254;
Pred. No. 8.3e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/08/475,668A FILING DATE: 07-JUN-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.8%; Sco. 100.0%; Pred. No. c. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEE: Pennie & Edmonds LLP: 1155 Avenue of the Americas New York
                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                         7872-020
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 790-9030
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNTE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
                                                                                                                                                                                                                                                        NAME: COTUZZI, LBUTA A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 78; TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 35.8
Best Local Similarity 100.
Matches 86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
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ZIP: 10036-2711
                                                                                                                             FILING DATE:
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117 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNRFYRDRYYRNLNIAPAEDGY 176
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                                                                                                                                                                                                                                                                                                             APPLICANT: Barney, Stawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: MEMBRANE STORM SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 254;
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
GOREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485, 264A
FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
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8.3e-79;
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100.0%; Pred. No. 0...
0; Mismatches
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NAME: COLULAL, LAULA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
FELERAX: 6614 PENNER
INFORMATION FOR SEQ. ID NO: 114:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                               ; Sequence 114, Application US/08485264A
; Patent No. 6228983
; GENERAL INFORMATION:
                                                                                 177 RLAGFPPDHQAWREEPWIHHAPQGGG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 RLAGFPPDHQAWREEPWIHHAPQGCG 188
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                                                                                                                                                                                                                                                          Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
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Best Local Similarity 100.
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS: ADDRESSE: Pennie & 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-485-264A-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New YORA
CITY: New YORA
COUNTRY: USA
TE: 10036-2711
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US-08-485-264A-114
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US-08-474-349A-114
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APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES.
ADDRESSED: Pennie & Edmonds LLP
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                                                                                                                                                                                                   Gaps
                                                                                                                                        0;
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                                                                                                 Length 254;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/471,913A FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                               Query Match 35.8%; Score 86; DB 3; L
Best Local Similarity 100.0%; Pred. No. 8.3e-79;
Matches 86; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.8%; Score 86; DB 3; L
100.0%; Pred. No. 8.3e-79;
tive 0; Mismatches. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: COTUZZI, LGUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFAX: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC competible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                            Sequence 114, Application US/08471913A Patent No. 6093794 GENERAL INFORMATION:
                                                                                                                                                                                                                                                        163 RLAGFPPDHQAWREEPWIHHAPQGCG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bolognesi, Dani P. APPLICANT: Matthews, Thomas J. APPLICANT: Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-485-551A-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1155 A. CILY: New York
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Best Local Similarity
Matches 86; Conserva
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TOPOLOGY: lir
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                                                                                                             APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: PUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Burnette, W. Neal
APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.8%; Score 86; DB 4; Length 254; 100.0%; Pred. No. 8.3e-79; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER REAGABLE FORM:
MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOOKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
Sequence 114, Application US/08474349A Patent No. 6333395
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 RLAGFPPDHQAWREEPWIHHAPQGCG 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 790-9050
TELEFAX: (212) 865-9741/8864
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
                                                               Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
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amino acid
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Best Local Similarity 100.4
Matches 86; Conservative
                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                  E: New York
IRY: USA .
10036-2711
                                                                                                                                                                                                                                                                                                                                                                New York
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                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Patent No. 5874287
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Railow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.8%; Score 26; DB 2; Length 179;
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COUNTRY: USA
ZIP: 91320-1789

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/435,605A
FTIING DATE: 05-MAY-1995
                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.4e-18;
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Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/435,605A
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mazza, Richard J.
REGISTRATION NUMBER: 27,657
REFERENCE/DOCKET NUMBER: A-196B
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
STREET: '1840 De Havilland Drive CITY: Thousand Oaks STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Amgen Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 EYFDRGTQMNINLYDHARGTQTGFVR 54
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ATTORREY/AGENT INFORMATION:
NAME: MAZZA, RICHARD J.
REGISTRATION NUMBER: 27,657
REFERENCE/DOCKET NUMBER: A-19(
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
                                                                                                                                   MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-435-605A-57
                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-435-605A-14
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COUNTRY:
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Patent No. 5874287
GENERAL INFORMATION:
APPLICANT: Burnette, W. Neal
APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08435605A
Patent No. 5874287
GENERAL INFORMATION:
APPLICANT: Burnette, W. Neal
APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                    Ouery Match 10.8%; Score 26; DB 2; Length 192; Best Local Similarity 100.0%; Pred. No. 1.5e-18; Matches 26; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: 1840 De Havilland Drive
STREET: 1840 De Havilland Drive
CTIY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIF: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: PEROPY disk
COMPUTER: PEROPY disk
COMPUTER: PENDER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,605A
FILING DATE: 05-MAY-1995
CLASSIFICATION: UNMBER: 27,657
REFERENCE/DOCKET NUMBER: 37,657
REFER
                                                                                                                                                                                                                                                                                                                                                             29 EYFDRGTQMNINLYDHARGTQTGFVR 54
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        protein
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; MOLECULE TYPE:
US-08-435-605A-8
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US-08-435-605A-14
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US-08-435-605A-6
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## ADDRESSET: 1840 De Havilland Drive
CITY: TROUGHOUSE ANGEN INC.
CITY: TROUGHOUSE ANGEN INC.
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Sequence 114, App
Sequence 6, App11
Sequence 6, App11
Sequence 4, App11
Sequence 50, App11
Sequence 52, App11
Sequence 52, App11
Sequence 52, App11
Sequence 3, App11
Sequence 3, App11
Sequence 2, App11
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Sequence I. Application US/09297171
SERERAL INFORMATION:
APPLICANT: Pizza, Mariagrazia
APPLICANT: Giuliani, Marzia M
APPLICANT: Giuliani, Marzia M
APPLICANT: Rappuoli, Rino
TITLE OF INVENTION: IMMUNOGENIC DETOXIFIED MUTANT E. COLI LT-A TOXIN
FILE REFERENCE: 0342.001 / 2302-0342
CURRENT APPLICATION NUMBER: US/09/297,171
CURRENT FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: PCT/IB97/01440
PRIOR APPLICATION NUMBER: PCT/IB97/01440
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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US-08-360-107-124

US-08-470-896-114

US-08-471-9114

US-08-475-668-114

US-08-484-223-114

US-08-485-546-114

US-08-485-546-114

US-08-485-546-114

US-08-485-551-114

US-08-485-551-114

US-08-487-266-114

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US-08-919-600-114

US-08-919-600-114

US-08-919-917-6

US-09-919-917-8

PCT-US99-30747-46

PCT-US99-30747-52

US-09-470-124-46

US-09-470-124-50

US-09-365-530-2

US-09-470-124-50

US-09-365-530-2

US-09-365-530-2

US-09-365-531-12-12-12
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US-09-051-315-2
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113
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6
114
22
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18
18
18
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US-09-297-171-1
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240; Conserv
                                               LENGTH: 240
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   Query Match
Best Local Si
Matches 240;
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Sequence 3, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 6, Appli
Sequence 2, Appli
                                                                                                   June 10, 2002, 17:35:19 ; Search time 107.44 Seconds (without alignments) 786.256 Million cell updates/sec
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                                                                                                                                                                                              1 NGDRLYRADSRPPDEIKRSG.....QIFSDYQSEVDIYNRIRDEL
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1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/USO6_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/USO6_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/USO8_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/USO8_COMB.pep:*
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7: /cgn2_6/ptodata/2/paa/USO8_COMB.pep:*
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16: /cgn2_6/ptodata/2/paa/USO8_COMB.pep:*
16: /cgn2_6/ptodata/2/paa/USO9_COMB.pep:*
16: /cgn2_6/ptodata/2/paa/USO9_COMB.pep:*
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18: /cgn2_6/ptodata/2/paa/USO9_COMB.pep:*
19: /cgn2_6/ptodata/2/paa/USO9_COMB.pep:*
20: /cgn2_6/ptodata/2/paa/USO9_COMB.pep:*
21: /cgn2_6/ptodata/2/paa/USO9_COMB.pep:*
22: /cgn2_6/ptodata/2/paa/USO9_COMB.pep:*
23: /cgn2_6/ptodata/2/paa/USO9_COMB.pep:*
24: /cgn2_6/ptodata/2/paa/USO9_COMB.pep:*
25: /cgn2_6/ptodata/2/paa/USO9_COMB.pep:*
26: /cgn2_6/ptodata/2/paa/USO9_COMB.pep:*
26: /cgn2_6/ptodata/2/paa/USO9_COMB.pep:*
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                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-256-003-3
PCT-US99-30747-4
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US-09-044-696-2
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US-09-819-917-7
                                                                                                                                                                                                                                                                        3502263 seqs, 351980561 residues
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                                                                         OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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length: 2000000000
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Scoring table:

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                                                                                                                             121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                              121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
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                                                                                                                                                                                                                                                                   APPLICANT: Domenighini, Mario
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
TITLE OF INVENTION: Immunogenic Detoxified Mutants of
TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their ITTLE OF INVENTION: Their Use for the Preparation of Vaccines
NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,003
FILING DATE: 11-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 188; DB 6; Le
Pred. No. 1.1e-185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.3%; Scc. 100.0%; Pred. No. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0315.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510, 661-2708
TELEFAX: (510, 665-3542
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
                                                                                                                                                                                                                                           Sequence 3, Application US/08256003 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
"MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 amino acids
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California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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CITY: Eme
STATE: Ca
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FILE REPERENCE: 4868/8447
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT FILING DATE: 1999-12-22
SUFRENT FILE REPERENCE: 2099-12-22
SOFTWARE: PATCHIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mason
APPLICANT: Mason
APPLICANT: Arntzen
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed In
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/84454
CURRENT APPLICATION NUMBER: US/09/470,124
CURRENT FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 YGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description of Artificial Sequence:E. coll heat-labile toxin gene mutagenized to optimize expression in plants.
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                                               Sequence 4, Application PC/TUS9930747 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09470124 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 184; Conserv
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OTHER INFORMATION:
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RESULT 3
PCT-US99-30747-4
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103 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGY 162
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GENERAL INFORMATION:
APPLICANT: BARCHEELD, GAIL
APPLICANT: DEL GIUDICE GUSEPPE
APPLICANT: RAPPOOLI, RINO
TITLE OF INVENTION: ADP-RIBOSYLATING TOXINS AS PARENTERAL ADJUVANTS
TUTLE OF INVENTION: ADP-RIBOSYLATING TOXINS AS PARENTERAL ADJUVANTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE CHIRON CORPORATION, INTELLECTUAL PROPERTY
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hes 0; Indels
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APPLICATION NUMBER: US/09/044,696
FILING DATE: 18-MAR-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,227
FILING DATE: 21-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                     ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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100.0%; Pred. No. c.
.. 0; Mismatches
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FILING DATE: 11-NOV-1994
CLASSIFICATION: 435
ATTOCKNEY/AGENT INFORMATION:
NAME: MCCLUNG, Barbara G.
REGISTATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0315.001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 510 (655-3542)
INFORMATION FOR SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
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CITY: EMERYVILLE
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-256-003-6
       Emeryville
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                         USA
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US-09-044-696-2
                                                         COUNTRY:
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GENERAL INFORMATION:
APPLICANT: Domenighini, Mario
APPLICANT: Rappuoli, Rioo
APPLICANT: Rappuoli, Rioo
APPLICANT: Pizza, Mariagrazia
TITLE OF INVENTION: Immunogenic Detoxified Mutants of
TITLE OF INVENTION: Cholera Toon and of the Toxin Lt, Their Preparation and
TITLE OF INVENTION: Their Use for the Preparation of Vaccines
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Sequence 7, Application US/09819917
Sequence 7, Application US/09819917
Sequence 7, Application
APPLICANT: Pizza, Mariagrazia
APPLICANT: Giancelli, Valentina
APPLICANT: Rapporoli, Wina
TILLE OF INVENTION: Immunogenic Detoxified Mutants Of Cholera Toxin
FILE REPERBENCE: CHRR0312
CURRENT APPLICATION NUMBER: US/09/819,917
CURRENT FILING DATE: 2001-03-28
PRIOR FILING DATE: 1997-12-22
PRIOR FILING DATE: 1995-06-30
SPRIOR FILING DATE: 1995-06-30
NUMBER, OF SEQ ID NOS: 8
SOFTWARE: Patentin Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 SLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPYSQI 143
                                                                                                                                                                                                                                                                                                                       81 STYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLH 140
                                                                                                                                                                                             65 SLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPYSQI 124
                                                                                                                                                                                                                                                                                           125 YGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAP 184
                                                                                                                            24 LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                         Gaps
                                                                                                 5 LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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    Length 259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 RNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQGCG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 RNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQGCG 188
                                                 Indels
  76.7%; Score 184; DB 18; L
100.0%; Pred. No. 1.6e-181;
iive 0; Mismatches 0;
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                                                 Matches 184; Conservative
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CORRESPONDENCE ADDRESS:
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 col1
                                                                                                                                                                                                                                                                                                                                                                                       185 QGCG 188
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STREET: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: E.
US-09-819-917-7
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FUSION-ASSOCIATED EVENTS, INCLUDING HIV
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                                                                                                                                                                                                               117 VYSPHPYEQEVSALGGIPYSQIYGWYRVNEGVIDERLHRNREYRDRYYRNLNIAPAEDGY 176
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APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Petteway, Stephen R.
APPLICANT: Mathonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUI
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
                                                                                                                                                     ó
                                                                                                          Length 254;
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                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER: EBADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOSANS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,896
FILING DATE: O6-UNN-1995
CLASSIFICATION: 435
ATTONNEY/AGENUT
                                                                                                   35.8%; Score 86; DB 7; Lv 100.0%; Pred. No. 5.4e-80; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                     163 RLAGFPPDHQAWREEPWIHHAPQGCG 188
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 114, Application US/08470896 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
                                                                                                 Query Match
Best Local Similarity 100.C
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
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Best Local Similarity 100.0
Matches 86; Conservative
                  protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
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                    ; MOLECULE TYPE:
US-08-360-107-124
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APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                    103 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                  35.8%; Score 86; DB 14; Length 236; 100.0%; Pred. No. 5e-80; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107
FILING DATE: 20-DEC-1994
CLASSIFICATION: 4355
CLASSIFICATION: 4355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                        1393.002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 RLAGFPPDHQAWREEPWIHHAPQGCG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 124, Application US/08360107 GENERAL INFORMATION:
NAME: HARBIN, ALISA A.
REGISTRATION NUMBER: 33,895
REFRENCE/DOCKET NUMBER: 1393.
TELECOMMUNICATION INFORMATION:
TELEPAX: (510) 655-8730
TELEFAX: (510) 655-8742
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn C.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 254 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                              Ouery Match 35.8
Best Local Similarity 100.
Matches 86; Conservative
                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-09-044-696-2
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ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS
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COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS TRANSMISSION
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APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Mid, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGY 162
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                                                                                                                                                                                                                                                                                                               COUNTRY USA

ZIP: 10036-2711

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668
FILLING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 35.8%; Score 86; DB 8; L
Best Local Similarity 100.0%; Pred. No. 5.4e-80;
Matches 86; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                    E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 RLAGFPPDHQAWREEPWIHHAPQGCG 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-(
TELEPHONE: (212) 790-9090
TELEPAX: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                              Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J
Matthews, Thomas J. Wild, Carl T.
                                       Barney, Shawn O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
                                                                                                                                                                                          NUMBER OF SEQUENCES: 209 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                     APPLICANT: Barney, St
APPLICANT: Lambert, I
APPLICANT: Petteway,
APPLICANT: Langlois,
TITLE OF INVENTION: C
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                                                                                                                                                                                                                                                                                                    New York
                                                                                                                                                                                                                                                                                New York
                                                                                                                                                                                                                                    ADDRESSEE:
STREET: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-475-668-114
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US-08-484-223-114
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APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913
FILING PATE: 07-JUN-1995
FILING PATE: 07-JUN-1995
FILING PATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8; Le
5.4e-80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7872-030
                                            177 RLAGFPPDHQAWREEPWIHHAPQGCG 202
                   163 RLAGFPPDHOAWREEPWIHHAPQGCG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 RLAGFPPDHQAWREEPWIHHAPQGCG 188
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US-08-475-668-114
Sequence 114, Application US/08475668
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
                                                                                                                                                                    Sequence 114, Application US/08471913 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 07-UNN-1995
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: COLUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFRENCE/DOCKET NUMBER: 7872-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFPAX: (212) 869-9741/8864
                                                                                                                                                                                                         APPLICANT: Bolognes1, Dani P. APPLICANT: Matthews, Thomas J. APPLICANT: Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 254 amino acids PYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-471-913-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                         RESULT 10
US-08-471-913-114
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APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Detteway, Stephen R.
APPLICANT: Detteway, Stephen R.
APPLICANT: Petteway, Stephen R.
APPLICANT: Petteway, Note The Common Petteway, Stephen R.
APPLICANT: Petteway, Stephen R.
APPLICANT: Denois Fusion-Associated Events, INCLUDING EPSTEIN-BARR VIRUS TITLE OF INVENTION: TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
TOWNERSPONDENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 254;
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APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546 FILING DATE: CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 8; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.8%; Score 86; DB 100.0%; Pred. No. 5.4 live 0; Mismatches
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-028
TELECHMUNICATION INFORMATION:
TELECHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
         CGRRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 RLAGEPPDHQAWREEPWIHHAPQGCG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 RLAGFPPDHQAWREEPWIHHAPQGCG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 114, Application US/08485546 GENERAL INFORMATION:
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                                                                                                                NAME: COLUZZI, LGUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-(
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
                                                  FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                     LENGTH: 254 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 35.8%
Best Local Similarity 100.0
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10036-2711
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STATE:
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APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Mild, Carl T.
APPLICANT: Mild, Carl T.
APPLICANT: Lambort, Dennis M.
APPLICANT: Lambort, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1¢3 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223 FILING DATE: 07-JUN-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. No. 5.4e-80;
E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 114, Application US/03484223A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 RLAGFPPDHQAWREEPWIHHAPQGCG 188
                                                                                                                                                                                                     PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USE ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
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Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                    COUNTRY: USA
ZIP: 10036-2711
                                                                    New York
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STRANDEDNESS:
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  ADDRESSEE:
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us-09-297-171-1.oligo.rapm

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APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
WUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                   111 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGY 176
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                                                                                                                                                                                                                                                                           Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONTESTONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER REAGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
COMPUTER: PatentIn Release #1.0, Version #1.30
COMPUTER: OT-JUN-1995
COMPUTER: OT-JUN-1995
COMPUTER: OT-JUN-1995
APPLICATION NUMBER: US/08/485,546A
FILING DATE: OT-JUN-1995
CLASSIFICATION: A35
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAUTA A.
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/COMPUTION INFORMATION:
TELEFRAX: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                     35.8%; Score 86; DB 8; L
Hlarity 100.0%; Pred. No. 5.4e-80;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-485-546A-114
Sequence 114, Application US/08485546A
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 RLAGFPPDHQAWREEPWIHHAPQGCG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bolognesi, Dani P. APPLICANT: Matthews, Thomas J. APPLICANT: Wild, Carl T.
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 254 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                    ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-485-546-114
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 86; Conserv
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Scoring table:

Sequence:

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Run on:

Word size :

Searched:

Database :

Result

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Gaps

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Length 240; Indels

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Sequence 3, Application US/09809033A
GENERAL INFORMATION:
APPLICANT: McGhee, Jerry
Klyono, Hiroshi
Takeda, Yoshifumi
Ohmura, Mari
Yamamoto, Shingo
TITLE OF INVENTION: Chimeric Nontoxic Mutants of
Humoral Immunity
                                                                                                                                                                                                                                                                                                                                                        61 STSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                 61 STSLSLRSAHLAGGSILSGYSTXYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 YSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 HHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
                                                                                                                                                                                                                                                            1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                            100.0%; Score 240; DB 5; L
100.0%; Pred. No. 1.5e-239;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/809,033A
FILING DATE: 16-Mar-2001
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: MGG-01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc
STREET: P.O. Box 2509
CITY: Fairfax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 703/425-8405
TELEFAX: 703/425-8406
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 382 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLGGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22031
COMPUTER READABLE FORM:
                                          TYPE: PRT
CRGANISM: Escherichia coli
US-09-528-682-1
                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 240; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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COUNTRY: U
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SEQ ID NO 1
LENGTH: 240
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1175.418 Million cell updates/sec
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Sequence 3, Appli
Sequence 4, Appli
Sequence 1083, Ap
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| Sequence 1. Application US/09528682
| Sequence 1. Application US/09528682
| GENERAL INFORMATION:
| APPLICANT: Pizza, Mariagrazia | APPLICANT: Giuliani, Marzia M | APPLICANT: Rappouli, Rino | APPLICANT: Rappouli, Rino | APPLICANT: Rappouli, Rino | APPLICANT: SPERENCE: 2302-0342.10 | CURRENT PILING DATE: 2000-03-20 | CURRENT FILING DATE: 2000-03-20 | PRIOR APPLICATION NUMBER: PGT/IB97/01440 | PRIOR APPLICATION NUMBER: PGT/IB97/01440 | PRIOR FILING DATE: 1997-10-30 | PRIOR FILING DATE: 1997-10-30 | PRIOR FILING DATE: 1999-04-27 | NUMBER OF SEQ ID NOS: 4 | SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                240
1 NGDRLYRADSRPPDEIKRSG......QIFSDYQSEVDIYNRIRDEL 240
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                                                                                                                                                              June 10, 2002, 17:35:44 ; Search time 15.66 Seconds
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1: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.ppp:*

2: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.ppp:*

3: /cgn2_6/ptodata/2/paa/USO7_NEW_COMB.ppp:*

4: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.ppp:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.ppp:*

6: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.ppp:*

7: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.ppp:*
                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-528-682-1
US-09-809-033A-3
US-09-809-033A-4
US-09-573-655B-1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                        233302 seqs, 76696041 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                 - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                     OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                          US-09-297-171-1
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Match Length DB
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382
382
814
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10.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
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RESULT , 4
JS-09-573-655B-1083
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LENGTH: 814
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                                                                                                                                      Gaps
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                                                                                                  Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 382;
                                                                                                Query Match 10.8%; Score 26; DB 5; Length 382
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 26; DB 5; Length 382
Pred. No. 1e-18;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DACA:
APPLICATION NUMBER: US/09/809,033A
FILING DATE: 16-Mar-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; STRANDEDNESS: single
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MYDOTHETICAL: NO
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGENT TYPE: N-terminal
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-809-033A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: McG-01
TELECOMMUNICATION INFORMATION:
; FRAGMENT TYPE: N-terminal ; SEQUENCE DESCRIPTION: SEQ ID NO: 3: US-09-809-033A-3
                                                                                               10.8%; Score 26; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc
STREET: P.O. Box 2509
                                                                                                                                                                                        47 EYFDRGTQMNINLYDHARGTQTGFVR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EYFDRGTQMNINLYDHARGTQTGFVR 72
                                                                                                                                                                     29 EYFDRGTQMNINLYDHARGTQTGFVR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EYFDRGTQMNINLYDHARGTQTGFVR 54
                                                                                                                                                                                                                                                       RESULT 3
US-09-809-033A-4
'Sequence 4, Application US/09809033A, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.8%; SCCL.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                         APPLICANT: McGhee, Jerry
Kiyono, Hiroshi
Takeda, Yoshifumi
Ohmura, Mari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 703/425-8405
TELEFAX: 703/425-8406
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 382 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Fairfax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: VA
COUNTRY: US
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Best Local Similarity
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Sequence 1083, Application US/09573655B
Sequence 1083, Application US/09573655B
Sequence 1083, Application US/0957365B
Sequence 1083, Application
TITE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptic.
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-0876P
CURRENT FILING DATE: 2000-05-18
CURRENT FILING DATE: 2000-05-18
SEQ ID NO 1083
LENGTH: 814
SEQ ID NO 1083
TYPE: RFT
CORGANIEM: Arabidopsis thaliana
SEQ ID NO 1083
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